

BASE COUNT 450 a 291 c 359 g 474 t
ORIGIN
Query Match 26.7%; Score 603; DB 6; Length 1574;
Best Local Similarity 75.7%; Pred. No. 5e-136;
Matches 890; Conservative 0; Mismatches 245; Indels 40; Gaps 10;
QY 169 GTGGTTTCCTGCTCCTCGACTACGACCTCTGCGGCGAGAGACTCTCCGGAATCCT 228
DB 24 GGCAATTCATGCCCTCCGAGCTCGAGCTCCTCGGGGAGAGACTCGAGAGCTCT 83
QY 229 CTCGGAGAGTCCGCGAGTGTCTCTCCGACATCGACTCCTCCTCCGCGCTC 288
DB 84 CACCGGAGATTACCGGATGCTCCTCCGACCTGGATTCATCATCGCACTGGCC 143
QY 289 GCCGACGACA-----GAGGATTGTATTCGATCGGAGCTTCATGAGACGA 336
DB 144 GTCTGCTCATTTATTTGCCGAGAGAGAGAGATTCGATGCTGTTTTCATGAGACGA 203
QY 337 GCGCAACTTCGTTCCGGGATTCGAGTACCTGTCGGGTTCAATCTCGCTCCGAGCG 396
DB 204 GTTCAAGTTTGTCTCTGCTGTTGACTATGTCTCAAGATTCCATCTCGCTCTCGAATC 263
QY 397 CAACGCCAGAGAGATCATGTTGATGATTCCTCAAGGTACAGCGGTACTATGGCTTCA 456
DB 264 CAGCACAGAGAGAGAGATTCATGATGATTCCTCAAGGTACATGATGATGATGATTC 323
QY 457 GCTTTGACGGGCTACCTCGCTCAACTATGATGATGATGATGATGATGATGATGAT 516
DB 324 GCGGTTAACGGGCTACCTCGCTCAACTATGATGATGATGATGATGATGATGATGAT 383
QY 517 GGC-GGAACAAATGGGCTCGCTCGACATGATGATGATGATGATGATGATGATGAT 575
DB 384 ACCGGGAAATGAGATGAGGACCTGACACTTTTATCTGTTGATGATGATGATGATGAT 443
QY 576 CAAGATGAGAGACCTCTGTTCCATCTCTGTTGACCTCAGATGAGAGGTGCCAAT 635
DB 444 CAAAGATG-GAGACACATGGTTCTCTCTCTGTTGACCTCAGATGAGAGGTGCCAAT 502
QY 636 ACATATTTGAGCGGAGACAAATTCGATGATGATGATGATGATGATGATGATGAT 695
DB 503 ACATATTTGACCGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 562
QY 696 GAGGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 755
DB 563 GAGGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 619
QY 756 CAACCTGACCTTTATCCGGTTCATTTCCAGGCGACAGAGAAATCATGATCTAATA 815
DB 620 TCATCTGAACTTTCAACCACTTCATATTTCAAGTGTACAGAAATCATGATCTAATA 679
QY 816 TCCAGAGGCTAGCTTTCTGCTTACTGCGCTTCATGATGATGATGATGATGATGAT 875
DB 680 TCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 739
QY 876 CTGACACTAATGAATTCCTAATTTGCTGTGTGAAGCCGAAATGCTGATGATGAT 935
DB 740 CTGACACTAATGAATTCCTAATTTGCTGTGTGAAGCCGAAATGCTGATGATGAT 799
QY 936 GCGAGGAGCTAAGAAAGAAAGTAAAGGCTACCGCTGATGATGATGATGATGATGAT 995
DB 800 GTGAAGAGCTAAGCAAGAAAGAAATTAAGGCTATGATGATGATGATGATGATGAT 859
QY 996 TTAAACATATACCAAGGAAATCCCTTACTAAAGTGTGCGGACCTCGAGTACAA 1055
DB 860 GTAGCAATACCGAGAAATGCCCC-----GAAAGTGTGCGGACCTCGAGTACAG 913
QY 1056 CTGGAACCGGATAGGTCAAGT-----ACTGATCATCATTCATCATCTCTT 1106
DB 914 CTGGAACCGGATAGGTCAAGT-----ACTGATCATCATTCATCATCTCTT 973
QY 1107 CAACCTCTTCTCTCTCTCTCTGTAAGAGAGAAATTAATACCGTTTGTGGTAA-- 1164

DB 974 CACCTCTTACTCGTTGCTTATAAAGAGAAATTAATAGCTGTTCTGGTAGATG 1033
QY 1165 -TGACAAAGAGAAATCCGAGTCAAGAGAAAGCAACATTAATTAAGAGAGAGA 1223
DB 1034 TTGACAAAGAGAAATTCAGAGGAGAGAGAAAGAAACAAAGATTAATA---ATPAAG 1089
QY 1224 AAGAGAGGATTAAGTGGGCGCAAGTTGTCTAGAAGACCTCAATTTTATGAGGCTT 1283
DB 1090 AACAAGAGAGAAATTAAGTGGGCGAGAGTTGTCTAG-AACCTCAACATTTTAAAGAGCTT 1148
QY 1284 TTGCAATTAATAATGACTTGAAGTAGAGGCTTGA 1318
DB 1149 TTGCAATTAATAATTTGACTATATGTTGATGATATA 1183
RESULT 2
A85060 1788 bp DNA linear PAT 21-JAN-2000
LOCUS A85060
DEFINITION Sequence 4 from Patent WO9842851.
ACCESSION A85060
VERSION A85060.1 GI:6733801
KEYWORDS
SOURCE
ORGANISM
Helianthus tuberosus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
REFERENCE
1 (bases 1 to 1788)
Murray J.A.
PLANTS WITH MODIFIED GROWTH
PATENT: WO 9842851-A 4 01-OCT-1998;
MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
FEATURES
source
1..1788
/organism="Helianthus tuberosus"
/db_xref="taxon:4233"
BASE COUNT 511 a 386 c 387 g 504 t
ORIGIN
Query Match 16.8%; Score 379.8; DB 6; Length 1788;
Best Local Similarity 72.5%; Pred. No. 1.3e-81;
Matches 492; Conservative 0; Mismatches 187; Indels 0; Gaps 0;
QY 307 TTATTCGATCGGAGCTTCATTCGAGCAGAGCCAACTTCGCGGATTCGAGTACT 366
DB 284 TGATTCGATCGGAGCTTCATTCGAGCAGAGAAAGTTGCTCCAGATTCATTAAT 343
QY 367 GTGCGGTTCCAAATCTCGCTCCCTGAGCGCAAGCCAGAGAAATCACTGGATGAT 426
DB 344 CGAGCGATTCATTCGCAAGTTCTCGATGCTTCGTAGAGAGAAATCGGTTCCGAT 403
QY 427 TCTCAAGTACACGCTACTATGAGCTTTCAAGCTTTGACGGGCTACTCGCGTCACTA 486
DB 404 CTTAAGGTCGAACGCTTTTACGATTTCAAGCGGTTGACCGGCTTCCGCTTCACTA 463
QY 487 TATGATCGGTTTGTGATTCCTGCGCGTTGCCGAAACAAATGAGGCGCTCGCACT 546
DB 464 TCTGATCGGTTTGTGATTCCTGCGCGTTGCCGAAACAAATGAGGCGCTCGCACT 523
QY 547 TGTATCGTTCGATGCTTGTGCTTTGGCAGCAAGATGAGAAACCTTTGTCATCT 606
DB 524 CTATTCGTTCGATGCTTGTGCTTTTACCTGCTAAATGAGAGAAACCTTTATCTCTAT 583
QY 607 CTTCGACCTTCAGATTAAGGTGCGCAAGTACATATTTGACCGGAGAAATTCGTAGAT 666
DB 584 TCTTCATCTCCAGGTTAAGGTGCGCAAGTATATTTGAGCGGAGAAATTCGAGAAAT 643
QY 667 GGAAGTACTGTTCTCGGTCTTATGATGAGGCTTAAGTCACTAACACCATTTGCTT 726
DB 644 GGAAGTACTGTTCTCGGTCTTATGATGAGGCTTAAGTCACTAACACCATTTGCTT 703
QY 727 CTTGCTTTCTTCTGCGTCAAGATGATGATGATGATGATGATGATGATGATGATGAT 786

Db 704 TATCGCTTCTTTGCGACAAATGATCATCTGGAATGATACGGTTTCCTTATCTC 763
Oy 787 CAGGCAACAGAAATCATCTGATCTAATATCCAGAGCTAGCTTTCTTCTACTGCGC 846
Db 764 AAGGCAACACAAATATCTCTCAATATTCAGAGCTAGTTACTTGTGATTTGGC 823
Oy 847 TTCAATGATCTGCTGACGACATCTACATCTAATGAATCTTAAATCTGCTGT 906
Db 824 ATCATGATCTGCTGACGACATCTGCTGACGACATCTTCTTAAATCTGCTACT 883
Oy 907 GGTTAGCCCGCAAAATGCTGAGTCTGCTGCGAGGCTAAGAAAGAAAGTAATAG 966
Db 884 TATCAATGCTGATCATCTGATCATCTGCTGATGCTGATGCTTACGAAAGAGATCACA 943
Oy 967 GTGCTACCACTTGATGCAA 985
Db 944 ATGTACAGACTTGTACAA 962

RESULT 3
ATCD1 1951 bp mRNA linear PLN 25-MAR-1998
LOCUS A.thaliana mRNA for cyclin delta-1.
DEFINITION X83369
ACCESSION X83369.1 GI:2995129
VERSION cyclin; cyclin delta-1.
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 1951)
Soni,R., Carmichael,J.P., Shah,Z.H. and Murray,J.A.
A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif
Plant Cell 7 (1), 85-103 (1995)
JOURNAL 95210930
MEDLINE 2 (bases 1 to 1951)
REFERENCE Murray,J.A.H.
AUTHORS Direct Submission
JOURNAL Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
REMARK 3 (bases 1 to 1951)
Murray,J.A.H.
REFERENCE Direct Submission
AUTHORS Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of
Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
COMMENT On Mar 28, 1998 this sequence version replaced gi:605504.
FEATURES
source
1..1951
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/variety="ecotype Landsberg erecta"
/db_xref="taxon:3702"
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/clone_lib="PFL61"
/dev_stage="seedlings, stage 2 leaves"
104..1111
/codon_start=1
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/protein_id="CA58285.1"
/db_xref="gi:2995130"
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FEAKTIKMLVLYSLVDMRLSVTPDFISFEPAKIDPQCTPLSGPISNAETIILN
IKEASFLEYWSSSTAAAILLCVANEPLSLSVVPHSPSPKIDGLSKETKIVCTRLM
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N"
misc_feature 134..283

Query Match 16.7%: Score 377.2; DB 8; Length 1951;
Best Local Similarity 68.7%: Pred. No. 5.0e-81;
Matches 552; Conservative 0; Mismatches 243; Indels 9; Gaps 2;
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167..181
misc_feature /note="LXCXE motif"
344..361
misc_feature /note="cyclin box"
860..898
misc_feature /note="pept motif, potential"
1019..1051
BASE COUNT 535 a 327 c 451 g 638 t
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Oy 297 CAGAGATTTGTTATTCGATCCGAGCTTCATCGACAGACGACGACGACGAT 356
Db 240 CATGGCCGTGGATTCATCTGCTGTTTATCGAAGACGACGACGATCTGCTG 299
Oy 357 TCGAGTACCTGTCGGGTTCCAAATCTGCTCCCTGACGCCCAACGACGACGAT 416
Db 300 ATGATTTATCTCTGATGATTCGAACTCGATCTGATGCTGCTGCTGATGAT 359
Oy 417 TTGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 476
Db 360 TCGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419
Oy 477 CCGTCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 536
Db 420 CCGTCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479
Oy 537 CTGTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596
Db 480 CAATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 539
Oy 597 TTGCATCTCTTGGACCTTGCATGATGATGATGATGATGATGATGATGATGAT 656
Db 540 TTCCCTCTCTTGGACCTTGCATGATGATGATGATGATGATGATGATGATGAT 599
Oy 657 TTGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 716
Db 600 TAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 659
Oy 717 CACTTGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 776
Db 660 CGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719
Oy 777 TCTTATTTCCAGGCAACAAATTCATGATGATGATGATGATGATGATGATGATGAT 836
Db 720 TCTTATTTCCAGGCAACAAATTCATGATGATGATGATGATGATGATGATGATGAT 779
Oy 837 CTTAGTCT 896
Db 780 AGTACTGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 839
Oy 897 ATTGCT 950
Db 840 CTCTATCT 899
Oy 951 AAGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1010
Db 900 AAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959
Oy 1011 GGAATCT 1067
Db 960 TAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019
Oy 1068 TGAGTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1091
Db 1020 CAAGGCCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1043

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RESULT 4
AMA250396      1162 bp  mRNA  linear  PLN 15-NOV-1999
LOCUS          Antirrhinum majus mRNA for cyclin D1 (cyclD1 gene).
DEFINITION    AJ250396
ACCESSION    AJ250396.1  GI:6448479
VERSION      cyclD1 gene: cyclin D1.
KEYWORDS      snappdragon.
SOURCE        Antirrhinum majus
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.
REFERENCE     1 (bases 1 to 1162)
              Gaudin, V., Lunnese, P., Robert, P., Towers, M., Riou-Khamlich, C.,
              Murray, J., Coen, E. and Doonan, J.H.
              The expression of D-cyclin genes define distinct developmental
              zones in Antirrhinum apical meristems and is locally regulated by
              the cycloidea gene
TITLE         Unpublished
JOURNAL       2 (bases 1 to 1162)
REFERENCE     Doonan, J.H.
AUTHORS       Direct Submission
TITLE         Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Innes
JOURNAL       Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM
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              MELVLVRLVMDRLRSISPCVSLFPALKIDPGTGTGFTSPAKIILISTVOESLIE
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BASE COUNT   333 a 268 c 246 g 315 t
ORIGIN
Query Match      14.5%; Score 328.4; DB 8; Length 1162;
Best Local Similarity 64.6%; Pred. No. 4.1e-69;
Matches 548; Conservative 0; Mismatches 276; Indels 24; Gaps 3;
QY 382 TCGCTCCCTGGACGCCAACGCCAGAGAGATCAGTTGATGATTCGAAAGTACACGC 441
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DB 336 TCAATCCGTTGATTCCTTCTACTAGAACAGATCTACCGCATGATCCTCAAGTGCAACG 395
QY 442 GTACTATGGCTTTCAGCCTTTGACGGCGTACCTCGCCGTCACTATATGATCGGTTTTT 501
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DB 396 TTTATAGGGTTTTCAGCCGCTTAACGGCGTATCTCGCCGTTAGCTTTCGATCGTTTTCT 455
QY 502 GATATTCGCGCGGTGCGCGGAACAATGGGTGGCTCTGCACTGTATCTGTTCGATG 561
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DB 456 AANCGCCATCATCTGCGCAAGTTGAATGGGTGGCCAAATGCAACTATGTGCGTTGCGTG 515
QY 562 CTTGTCTTTGGCAGCAAGATGGAAGAACCTCTTGTTCATCTCTCTGACCTTCAGAT 621
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DB 516 CTTGTCTATGAGCTGTAAGATGAGAGAACTCTGTTCCCTCTCTTTGGATCTTCAGGT 575
QY 622 AGAAGTGCCAAATACATATTTAGCCGAGAACATTCGTAAGATGAGACTACTTGTCT 681
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DB 576 GGAAGGAGCAAACTTTATTTTAAACCAAAATATCCAAAGATGAGACTCTTCTGTGCT 635
QY 682 CGGTGCTTATGATGAGGCTAAGATCAGTAACACCACTTGTGCTCTGCTTCTTCTTGG 741
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DB 636 TAGGTTTATGATGAGACTTTCGGTCAATATCTCCATTTTGTATCTAGCTTTTTCGC 695

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QY 742 GTCAAAAGTAGATTCACACTGGAACTTTTATCCGGTCTCTTTTCCAGGGCAGCAAAAT 801
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DB 696 ACTCAAAATGCAACCCCACTGGAACTATACAGGTTTCTTGACGTCACAGGGCTAAAGAAAT 755
QY 802 CATGCTATCTAATATATCAAGAGGCTAGCTTTCTTGTCTTACTGCGCTTCATGATGCTGC 861
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DB 756 TATCTCTCAACCCGTTCAAGAGACCAAGTTGATGAGATATGCGCATCATGCTATGCTGC 815
QY 862 TGCACCCATPACACTGAGCTATGAAATTCATATGAGCTGTGGTTAGCCCGCAAA 921
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DB 816 TGCACAAATGCTTTTATGATGCGCAAAATGATCTGCCAAATTTTCTTCACTACTGCTCA 875
QY 922 TGTGAGTATGAGTGCAGGAGCTAAGAAAAGAAAAGTAATAGAGTCTACCAAGTAT 981
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DB 876 TGTGAGGAGATGCTGTGATGAGCTTCAACAAAGATATATGCTAGTTCATGATCAAACTGAT 935
QY 982 GCAGAGCTTGTGATTAACATATACCAACGGAAGTCCCTTACTTAAAGTGTGCGCA 1041
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DB 936 TCMAAGAGTGGAGTCAAAATAGGCCCAAAAAGACAGGCC-----AAGGTTTACACA 989
QY 1042 GCTGCGAGTAACAACTCGGACCCGAAATGAGGCAAGTCTATATCATTCATCATC 1101
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DB 990 GCTCGGATGATGACTCGGCGGAGTTTGCCCTCGAGT-----GAATGCTC 1034
QY 1102 CTCTTCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1158
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DB 1035 ATCATCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1094
QY 1159 GGTATATGACAAAGAACTCCGAGTGAAGAAAAGCAACAAATATATTAAGAAAGG 1218
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DB 1095 GATATGACAAAGAGAGCTCTGATTAAGGGGTCTTAAATTAAGGATTAAGAAAAA 1154
QY 1219 AAGAAAAA 1226
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DB 1155 AAAAAAAA 1162

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RESULT 5
AB5058      1679 bp  DNA  linear  PAT 21-JAN-2000
LOCUS          Antirrhinum majus Sequence 2 from Patent WO9842851.
DEFINITION    AB5058
ACCESSION    AB5058
VERSION      AB5058.1  GI:6733799
KEYWORDS      common tobacco.
SOURCE        Nicotiana tabacum
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
REFERENCE     1 (bases 1 to 1679)
              Murray, J.A.
              PLANTS WITH MODIFIED GROWTH
              Patent: WO 9842851-A 2 01-OCT-1998;
              MURRAY JAMES AUGUSTUS HENRY (GB); UNIV CAMBRIDGE TECH (GB)
TITLE         Location/Qualifiers
JOURNAL       1..1679
              /organism="Nicotiana tabacum"
              /db_xref="taxon:4097"
BASE COUNT   537 a 281 c 293 g 568 t
ORIGIN
Query Match      6.8%; Score 152.6; DB 6; Length 1679;
Best Local Similarity 52.2%; Pred. No. 3e-26;
Matches 338; Conservative 0; Mismatches 309; Indels 0; Gaps 0;
QY 372 GGTCCATCTCGCTCCCTCGAGCGCAAGCCAGAGAAATCAAGTGGATGATTCCTCA 431
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DB 455 GTTTTCAAGATGACCTTACTCTGTTCTGCCCGTGTGATGATCTGTGGAATGATTTTAA 514
QY 432 AGTACAGCGGACATATGAGCTTTAGCCTTTGAGCGGCTTACCTGCGGTCAACATATAG 491
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DB 515 AAGTAATGAGTATATATGAGTTTCTGCTTGTGACTGCGGTTTATGACCAATTAATTA 574

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RESULT 7
LOCUS      AB015222
DEFINITION Nicotiana tabacum NtCYCD3-1 mRNA, complete cds.
ACCESSION  AB015222
VERSION     AB015222.1
KEYWORDS   GI:4586800
SOURCE     Nicotiana tabacum cell_line:BY-2 cDNA to mRNA.
ORGANISM   Nicotiana tabacum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

REFERENCE  1 (bases 1 to 1487)
AUTHORS   Sekine,M.
TITLE      Cell cycle regulated gene
JOURNAL    Published Only in database (1999) In press
REFERENCE  2 (bases 1 to 1487)
AUTHORS   Sekine,M.
TITLE      Direct Submission
JOURNAL    Submitted (03-JUN-1998) Masami Sekine, Nara Institute of Science
            and Technology, Graduate School of Biological Sciences, Takayama
            8916-5, Ikoma, Nara 630-0101, Japan
            (E-mail:sekine@bs.ist.nara.ac.jp, Tel:+81-743-72-5462,
            Fax:+81-743-72-5469).
            Sequence updated (19-Aug-1998).

COMMENT    location/Qualifiers
FEATURES   location=1..1487
SOURCE     /organism="Nicotiana tabacum"
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BASE COUNT 462 a 257 c 287 g 481 t
ORIGIN
Query Match 6.4%; Score 143.8; DB 8; Length 1487;
Best Local Similarity 52.2%; Pred. No. 4.2e-24;
Matches 319; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 408 AAGATCACTGGATGATTCAGAGTACAGCGCTACTAGCGCTTTGACGCG 467
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Db 401 AAGAGCTGTGAAGATCTTAAGTCAATATGATGATTCACACATTCAC 460
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QY 468 CGTACCTGCGCTGCACTATGATGATGATGATGATGATGATGATGAT 527
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QY 528 ATGGTGCGCTGCACTATGATGATGATGATGATGATGATGATGATGAT 587
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Db 521 ACCCTTGATGATCACTGATGATGATGATGATGATGATGATGATGAT 580
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QY 588 AACCTCTTTTCCATCTCTCTTGGACCTTCAGATGAAAGGTCACAGTAT 647
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Db 581 AAATCCAGTCTCTCTCTTGGACCTTCAGATGAAAGGTCACAGTATG 640
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QY 648 CGAGAACATTCGTAGAGTGAAGTACTGTTCTGGGTGCTTAATGAGGCT 707
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QY 708 CAGTAACACCACTTGGCTTCGCTTCCTTTCGTCGCAAGTAGATCACTG 767
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Db 701 CTGTAACCCACCTTCACTTATTTGATCATATATTAAGAGACTTGGGCTAA 760
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Db 761 TACACTGGGAATTTCTTCACAGAGTGCAGAAATTTCTTTTGGTCATAG 820
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QY 888 AATTTCTTAATTTGCTGCTGTTAAAGCCGCAATGCTGATGCTGAGGACT 947
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Db 881 AAGTTGAGCCTTTGAATGCTGCTGATCAACCAATATCACTTGTGATTC 940
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QY 1008 AAGGGAAGTC 1018
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RESULT 8
LOCUS      AMA250397
DEFINITION Antirrhinum majus partial mRNA for cyclin D3a (CYCD3A gene).
ACCESSION  AJ250397
VERSION     AJ250397.1
KEYWORDS   CYCD3A gene; cyclin D3a.
SOURCE     snapdragon.
ORGANISM   Antirrhinum majus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Lamiales; Veroniceae; Antirrhinum.
            1 (bases 1 to 1140)
            Gaudin,V., Lunness,P., Robert,P., Towers,M., Rlou-Khamlichl,C.,
            Murray,J., Coen,E. and Doonan,J.H.
            The expression of D-cyclin genes define distinct developmental
            zones in Antirrhinum apical meristems and is locally regulated by
            the cycloidea gene
            Unpublished
            2 (bases 1 to 1140)
            Doonan,J.H.
            Direct Submission
            Submitted (18-OCT-1999) Doonan J.H., Cell Biology, John Innes
            Centre, Colney Lane, Norwich, NR4 7UH, UNITED KINGDOM
            location/Qualifiers
            1..1140
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BASE COUNT 332 a 223 c 237 g 348 t
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 BASE COUNT 554 a 283 c 308 g 552 t 2 others
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 Best Local Similarity 52.2%; Pred. No. 4,7e-20;
 Matches 307; Conservative 0; Mismatches 278; Indels 3; Gaps 1;

DEFINITION Lycopersicon esculentum mRNA for D-type cyclin.
 ACCESSION AJ002590
 VERSION AJ002590.1 GI:6434200
 KEYWORDS 3 gene; cyclD3; D-type cyclin.
 SOURCE tomato.
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eunasterids I; Solanales; Solanaceae; Solanum;
 Lycopersicon.
 1 (bases 1 to 1449)
 Kvarnheden, A., Yao, J. L., Zhan, X., O'Brien, I., and Morris, B. A. Isolation of three distinct cyclD3 genes expressed during fruit development in tomato.
 J. Exp. Bot. 51 (352), 1789-1797 (2000)
 JOURNAL 1113158
 PUBMED 2 (bases 1 to 1449)
 REFERENCE Kvarnheden, A.
 AUTHORS Direct Submission
 TITLE Submitted (11-NOV-1997) Kvarnheden A., Mt Albert Research Centre, The Horticulture and Food Research Institute of New Zealand, Private Bag 92169, Auckland, NEW ZEALAND
 JOURNAL Location/Qualifiers
 FEATURES
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 101..1111
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 Best Local Similarity 51.4%; Pred. No. 3.9e-19;
 Matches 314; Conservative 0; Mismatches 291; Indels 6; Gaps 1;

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Db 696 TGAAGCACTGCTATCTTTGGAATTTCTGAGGAGATGTGAGAAAGCTTCTTTACACAA 755
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OY 876 CTGAGCTATGAAATTCCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935
Db 816 ATGCTTGTAGAGCTTACGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 875
OY 936 GCGAGGAGCTAAGAAAGAAAGTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 995
Db 876 TTCTGGAATTCGAAAG 935
OY 996 TTAACAAATAC 1006
Db 936 GCAACATTTGAC 946

RESULT 15
LOCUS ATCD3 1632 bp mRNA 11nmer PLN 25-MAR-1998
DEFINITION A.thaliana mRNA for cyclin delta-3.
ACCESSION X83371
VERSION X83371.1 GI:2995133
KEYWORDS cyclin; cyclin delta-3.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; code eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1632)
Soul, R., Carmichael, J.P., Shah, Z.H. and Murray, J.A.
A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif
Plant Cell 7 (1), 85-103 (1995)
95210930
2 (bases 1 to 1632)
Murray, J.A.H.
JOURNAL Direct Submission
MEDLINE Submitted (08-DEC-1994) J.A.H. Murray, Inst. of Biotechn., Univ. of
AUTHORS Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
TITLE revised by [3]
REMARK 3 (bases 1 to 1632)
REFERENCE Murray, J.A.H.
AUTHORS Direct Submission
TITLE Submitted (19-MAR-1998) J.A.H. Murray, Inst. of Biotechn., Univ. of
JOURNAL Cambridge, Tennis Court Road, Cambridge, CB2 1QT, UK
COMMENT On Mar 28, 1998 this sequence version replaced g1:603508.
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Query Match 5.4%; Score 123; DB 8; Length 1632;
Best Local Similarity 50.4%; Pred. No. 5e-19;
Matches 300; Conservative 0; Mismatches 295; Indels 0; Gaps 0;
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BASE COUNT 478 a 369 c 317 g 468 t
ORIGIN

Db 636 GGAAGATGAATCCAGTAAACCCATTTTCATTTCTTGTATTTATTAAGTAAAGACTTGAT 695
OY 756 CAATGAGACCTTTATTCGGTTCCTTATTTCCAGGGGCAAGAAATCATGCTATTAAT 815
Db 696 TGAAGCACTGCTATCTTTGGAATTTCTGAGGAGATGTGAGAAAGCTTCTTTACACAA 755
OY 816 TCCAGAGGCTAGCTTTCTGCTTACTGCGCTTCATGATGCTGCTGCTGCGCATCTCA 875
Db 756 TTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 815
OY 876 CTGAGCTATGAAATTCCTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 935
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OY 936 GCGAGGAGCTAAGAAAGAAAGTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 995
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OY 996 TTAACAAATAC 1006
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Db 936 GCAACATTTGAC 946

Search completed: October 26, 2002, 01:34:54
Job time: 4150 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 22:39:44 ; Search time 366 Seconds
(without alignments)
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Title: US-09-665-308D-11

Perfect score: 2259

Sequence: 1 acaactctccacatc.....ttaaaaaaaaaa 2259

Scoring table:

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Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2259	100.0	2259	AAZ19958	soybean cyclin del
2	689.6	30.5	1994	AAZ19959	soybean cyclin del
3	388.4	17.2	1337	AAAC42423	Arabidopsis thalia
4	379.8	16.8	1788	AAV33887	Arabidopsis thalia
5	152.6	6.8	1679	AAV33885	N. tabacum CYCD3;1
6	134.4	5.9	1414	AAV33888	H. tuberosus CYCD3;
7	122	5.4	1311	AAAC40202	Arabidopsis thalia
8	120.8	5.3	1431	AAV33886	N. tabacum CYCD3;2
9	116.8	5.2	1284	AAV33884	N. tabacum CYCD2;1

10	116.2	5.1	1173	21	AAZ94583	Maize cyclin D ZMC
11	116	5.1	1356	21	AAZ51463	Arabidopsis thalia
12	116	5.1	1358	21	AAZ33723	Arabidopsis thalia
13	112.2	5.0	1846	19	AAV33889	Maize CYCD2 gene..
14	112.2	5.0	1861	21	AAZ94581	Maize cyclin D ZMC
15	110.6	4.9	1077	21	AAZ94582	Maize cyclin D ZMC
16	103.2	4.6	1932	20	AAZ19961	Arabidopsis thalia
17	99.4	4.4	1287	21	AAZ48840	Arabidopsis thalia
18	99.4	4.4	1290	21	AAZ3981	Arabidopsis thalia
19	97.8	4.3	927	20	AAZ36897	Arabidopsis thalia
20	87	3.9	1007	20	AAZ19956	Arabidopsis thalia
21	83.8	3.7	1734	21	AAZ94584	Arabidopsis thalia
22	59.6	2.6	1122	21	AAZ50081	Arabidopsis thalia
23	59.6	2.6	1721	21	AAZ50083	Arabidopsis thalia
24	55.8	2.5	1223	21	AAZ34444	Arabidopsis thalia
25	54.8	2.4	510	20	AAZ19957	Arabidopsis thalia
26	54	2.4	790	20	AAZ19963	Arabidopsis thalia
27	53.6	2.4	5525	24	AAZ34463	Human metastasis a
28	53.2	2.4	1732	21	AAZ38832	Arabidopsis thalia
29	51.8	2.3	17721	24	AAZ33729	Human immune syste
30	50.6	2.2	6076	24	AAZ32364	Human immune syste
31	50.6	2.2	6076	24	AAZ34480	Human metastasis a
32	50.2	2.2	5919	24	AAZ32388	Human immune syste
33	50.2	2.2	5919	24	AAZ61106	Human gene regulat
34	49	2.2	7849	24	AAZ22329	Chemically treated
35	48.6	2.2	9731	24	AAZ32890	Human immune syste
36	48	2.1	73334	24	AAZ34125	Human immune syste
37	47	2.1	5268	24	AAZ32876	Human immune syste
38	47	2.1	6161	24	AAZ61200	Human gene regulat
39	47	2.1	15881	24	AAZ32260	Human immune syste
40	47	2.1	15881	24	AAZ61069	Human gene regulat
41	47	2.1	18817	24	AAZ34495	Human immune syste
42	46	2.0	16287	24	AAZ32673	Human immune syste
43	45.8	2.0	6227	24	AAZ34499	Human metastasis a
44	45.8	2.0	10066	24	AAZ32037	Human immune syste
45	45.8	2.0	10710	24	AAZ32893	Human immune syste

ALIGNMENTS

RESULT 1	
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AC	AAZ19958;
XX	
AC	AAZ19958;
XX	
DT	21-DEC-1999 (first entry)
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DE	soybean cyclin delta-1 cDNA.
XX	
XX	Cyclin delta-1; soybean; cell cycle; cell division;
KW	transgenic plant; herbicide; plant breeding; ss.
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OS	Glycine max.
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PD	30-SEP-1999.
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PF	19-MAR-1999; 99WC-US06047.
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PR	23-MAR-1998; 98US-0078948.
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PA	(DUPO) DU PONT DE NEMOURS & CO E. I.
XX	
PI	Caboon RE, Klein TM, Odell JT, Orozco EM;
XX	
DR	WPI; 1999-591036/50.

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D	652	AATGAATTCCTTAATTTGGTCTGTCTCTGTAGCCGTGAGCTGCAAGATCTATGGTGTGAGGGG	711
Q	944	CTAAGAAAAAGAAAGTATATAGGGTCTACCAAGTGTGATGCAAGAGCTGTGATTACAAAT	1003
D	712	TTTAAAGAAAGGAAAAATTAAGGGGTGTCACAAATTAAGCAAGAACTGTGATTGACAAAT	771
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Q	1061	ACCCGATGAGGTCAAGTACTGATATCATTCTCATCATCTCTTCA---ACCTCTTC	1117
D	826	CCCATTAATGAGTCTAGTGTCTCATCTCTTCTTAGACATATCCTCTTCCACTTCATCATCC	885
Q	1118	TCCTTGTCTTGTGAAGAGGAGAAATTAATTAACCGTTTGTGGSTA---GATGACAAAGGA	1174
D	886	TCCTTGTCTTGTGAAGAGGAGAAATTAATACTTTGTGGGTGACATGACAAAGGA	945
Q	1175	AACCTCGATGAGAGAGAAAAACGACAACAACTATTAAGAAAGGAGAA-----AAA	1225
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D	1006	TAAGGTGTGGAGCGGGGTCCAAAGTTGTCCAGAAACCCGAAATTTTGTAAAGGGGTTTT	1065
Q	1286	GCAATTTAAAAATGACT---GAGTACGGGTGTAGATTATTAATAGATATATATGATATA	1342
D	1066	TTGAGATTAATAAGGATCTAGAGAGTGTGAGAGGTGACATTTAATATAGACTATATTTAAG	1125
Q	1343	TCCTATTCGATATACTAAGAGAGTTGATGGGTTGGAGTAATTTTATTTATATGTG	1402
D	1126	A-----GAGTTCGAGCTTTATTTATTTTGTGTGGG	1156
Q	1403	GTCACTTATTAATTAATGAGTTTGCAGAAATTCACCTAGGAGAGGAGATTTTGCACATGT	1462
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D	1371	TTTCAGACTCTTGGAAGAAAGAAAAAGCATAGTCTCAGAGAGAGATCAATATAGGATTATGA	1430
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D	1431	AAG-----ACTTTGAAGTTGAGCTGTGTTCTTCTTATATATATAGGGGTCTCTAAGTCAG	1485
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D	1486	CTACTCATCTTTGGGCA--GCATGCGCTGCTTCTTAGATTACAGCTTACTTTTGGTAGTGT	1544
Q	1823	GATGGGACCTTCAACAGTAAAGAACAATTTGAAGGCAATTAAGTTGAAGTTTGGCTACAAA	1882
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Q	1883	TCGTGACATTTTGTGTGGGTATTTGGCAGCTGTGCAGCTGCTGTGCTGCTGCCAATG	1942
D	1604	TTGTGGATTTATGATGATACCTGT-----GAAACCCCTCTGGTGTGTCTCTCGC	1652

QY	1943	AAGGTGTACGTGTGATTTTCTTTTCTTGGTTTT-----TCCTTCCGGGAGCTCTTT	1996
QY	1943	AAGGTGTACGTGTGATTTTCTTTTCTTGGTTTT-----TCCTTCCGGGAGCTCTTT	1996
Db	1653	ACGTCCTACGTGTGATTTTCTTTTCTTGGTTTT-----TCCTTCCGGGAGCTCTTT	1712
QY	1997	ATATATTTTTCCTATTTTGGCCATGAGTTTGGCCCTAACATACAGACCTCCATGAC	2056
Db	1713	TTATTTCTTTATTTCTTTTGGCTTGACCTTTGGCCTTACTATACAGAA-TCCATTGCC	1771
QY	2057	TGCTGTCCGGCGCTGTGAAACACGCTATATATAGTTTATTTTAAAAACCTTGA	2116
Db	1772	TGGTGTCTCAGCC--GTCATGGAACACGCTCATAT-----GTTTTCAATTTTGGTTTGG	1825
QY	2117	ATTTTATTTTATTTGTTTCAAGAGAGGAAACCCCTCTT-----	2154
Db	1826	ATTTTTCATTTGTTTCTCAGAGAGAGAAACCCCTCTTGTCTTTTATAGTGCCTAT	1885
QY	2155	-----CACATAGGGGTAAAGCTCTTGGGCGCTTTTCCGTGTGCTGTATTTG	2205
Db	1886	TGGCTTTGGGGAATTTGGAGTAAAGGCCCTTGGGCGCTTTCTGTAGTCTTTATTG	1945
QY	2206	GATGATTAATATATATATGACACATATATTTCTTAAAAAATTTTAAAAA	2259
Db	1946	AATTCATTAATTAATGA-----CACTGTATATCTATTAATTTAAAAAATTTTAAAAA	1994
RESULT 3			
AAC42423			
ID	AAC42423 standard; DNA: 1337 BP.		
XX			
AC	AAC42423;		
XX			
DT	17-OCT-2000 (first entry)		
XX			
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 35500.		
XX			
KW	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification assay; signal transduction pathway;		
KW	metabolic pathway; promoter; termination sequence; ss.		
XX			
OS	Arabidopsis thaliana.		
XX			
PN	Ep1033405-A2.		
XX			
PD	06-SEP-2000.		
XX			
PF	25-FEB-2000; 2000EP-0301439.		
XX			
PR	25-FEB-1999;	99US-0121825.	
	05-MAR-1999;	99US-0123180.	
PR	09-MAR-1999;	99US-0123548.	
	23-MAR-1999;	99US-0125788.	
PR	25-MAR-1999;	99US-0126264.	
	29-MAR-1999;	99US-0126785.	
PR	01-APR-1999;	99US-0127462.	
	06-APR-1999;	99US-0128234.	
PR	08-APR-1999;	99US-0128714.	
	16-APR-1999;	99US-0129845.	
PR	19-APR-1999;	99US-0130077.	
	21-APR-1999;	99US-0130449.	
PR	23-APR-1999;	99US-0130510.	
	23-APR-1999;	99US-0130891.	
PR	28-APR-1999;	99US-0131449.	
	30-APR-1999;	99US-0132040.	
PR	30-APR-1999;	99US-0133407.	
	04-MAY-1999;	99US-0133484.	
PR	05-MAY-1999;	99US-0133485.	
	06-MAY-1999;	99US-0133486.	
PR	06-MAY-1999;	99US-0133487.	
	07-MAY-1999;	99US-0132863.	
PR	11-MAY-1999;	99US-0134256.	
	14-MAY-1999;	99US-0134218.	
PR	14-MAY-1999;	99US-0134219.	

PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0136021.
 PR 25-MAY-1999; 99US-0136392.
 PR 27-MAY-1999; 99US-0136782.
 PR 28-MAY-1999; 99US-0137222.
 PR 01-JUN-1999; 99US-0137528.
 PR 03-JUN-1999; 99US-0137502.
 PR 04-JUN-1999; 99US-0137724.
 PR 07-JUN-1999; 99US-0138094.
 PR 08-JUN-1999; 99US-0138340.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-01394750.
 PR 18-JUN-1999; 99US-0139753.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140635.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143624.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
 PR 16-JUL-1999; 99US-0144086.
 PR 19-JUL-1999; 99US-0144325.
 PR 19-JUL-1999; 99US-0144331.
 PR 19-JUL-1999; 99US-0144332.
 PR 19-JUL-1999; 99US-0144333.
 PR 19-JUL-1999; 99US-0144334.
 PR 19-JUL-1999; 99US-0144335.
 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144633.
 PR 20-JUL-1999; 99US-0144864.
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 PR 21-JUL-1999; 99US-0145088.
 PR 22-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145089.
 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
 PR 23-JUL-1999; 99US-0145218.
 PR 23-JUL-1999; 99US-0145224.
 PR 26-JUL-1999; 99US-0145276.
 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151530.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-01527070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
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 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159337.
 PR 14-OCT-1999; 99US-0159631.
 PR 14-OCT-1999; 99US-0159638.
 PR 14-OCT-1999; 99US-0159658.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.

PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161350.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 17.28; Score 388.4; DB 21; Length 1337;
Best Local Similarity 68.98; Pred. No. 8.4e-88;
Matches 565; Conservative 0; Mismatches 246; Indels 9; Gaps 2;

QY 297 CAGAGATTGTTATTCGCGAGCTTCATCGACGACGAGCGAAGCTTCGCGGAT 356
DB 289 CATGGCCGTGGATTCATTCCTGTTTATCGAAGAGAGCGTCACTCTCTCGTGGAC 348
QY 357 TCGAGTACGCTGCGGGTTCATTCGCTCCCTGGAGCGCAACGCCAGAGAGATCAG 416
DB 349 ATGATTAATCTCTAGATTTCAAACTGATCTCTGATGCTTCGCTAGAGAAATTCG 408
QY 417 TTGATGATTTCTCAAGGTACAGCGTACTATGGCTTCAGCCTTTGACGGCTCTCG 476
DB 409 TCGCATGATTTCTCAAGGTACAGCGTATTAATCTTCAGCGCTTAAAGCGGCTCG 468
QY 477 CCGCAATATATGATGATGATTTTGGATTCGCGCGGTTGGCGGAACAATGGGTGC 536
DB 469 CCGTAACTAATAGATGATGATTTTACGCTCTGCTGATTCGGAAGAGAGTGGTGGC 528
QY 537 CTGTCGAATTTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 596
DB 529 CAATGCAATTTTATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 588
QY 597 TTCCATCTCTCTGAGACCTTCAGATAGAAAGTGGCAAGTACATATTGAGCGAGAAC 656
DB 589 TTCCATCTCTCTGAGACCTTCAGATAGAAAGTGGCAAGTACATATTGAGCGAGAAC 648
QY 657 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 716
DB 649 TAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 708
QY 717 CACTTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
DB 709 CGTTGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAATG 768
QY 777 TCCTTATTTCCAGGCAACAGAAATCAGTATCTAATATCCAGAGAGCTAGCTTTCTG 836
DB 769 TCTTATATCCCATGCTACAGAGATTAATCTCTCAACATTAAGAGAGAGAGCTTTCTG 828
QY 837 CTTACTGGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 896
DB 829 ACTACTGGCTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 888
QY 897 ATTTGGC-----TGGGTTAGCCCGAAGATGAGTATGATGATGATGATGATGATG 950
DB 889 CTCATCTCTCTGTTCAATCCCGACAGAGAGCCCTGAGCTTGATGAGATTTAGCA 948
QY 951 AAGAAAAAGTAAATAGGCTCTACAGTGTATGATGATGATGATGATGATGATGATGATG 1010
DB 949 AAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1008
QY 1011 GGAAGCTCCCTTACTAAAGTGTGCGAGCTGCGAGTAA---CACTCGAGCCGAA 1067
DB 1009 TAAATACACCAAAAGTATAGCAAAAGCTTGAAGTATGATGATGATGATGATGAT 1068
QY 1068 TGAAGTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1107
DB 1069 CAAGGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1108

RESULT 4
AAV33887

ID AAV33887 standard; cDNA to mRNA; 1788 BP.
XX AAV33887;
AC
XX 25-JAN-1999 (first entry)
XX
XX H. tuberosus CYCD1;1 gene.
DE
XX D-type cyclin; growth; plant; cell-division control; phosphorylation;
XX CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;
KW root development; ds.
XX Helianthus tuberosus.
OS
XX
XX
XX W09842851-A1.
XX 01-OCT-1998.
PD
XX
XX 24-MAR-1998; 98MO-EP01701.
PF
XX 26-MAR-1997; 97EP-0302096.
PR
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
PA
XX Murray JAH;
PI
XX WPI; 1998-532012/45.
DR
XX
XX
XX Regulating growth and structure of plants by modulating protein that
XX controls cell division - specifically a D-type cyclin, and related
XX chimeric genes and transformed cells and plants, used to alter
XX growth rate, flowering, seed production etc.
XX
XX
XX Claim 14; p56-57; 75pp; English.
XX
XX This sequence represents the CYCD1;1 cDNA from Helianthus tuberosus which
XX encodes a D-type cyclin. The sequence can be used to alter the growth
XX characteristics or architecture of plants by altering the (functional)
XX level in the plant cells of a cell-division controlling protein that can
XX bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
XX Modulation of the cyclin gene is used to increase or decrease the growth
XX rate, provide faster germination, reduce time to flowering, increase the
XX number of flowers, seeds or fruits per plant, increase root development,
XX reduce height and to delay flowering in a range of plants, e.g. legumes,
XX grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
XX carnation, chrysanthemum, rose, tulip, etc.
XX
XX Sequence 1788 BP; 511 A; 386 C; 387 G; 504 T; 0 other;
SQ

Query Match 16.8%; Score 379.8; DB 19; Length 1788;
Best Local Similarity 72.5%; Pred. No. 1.4e-85;
Matches 492; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

QY 307 TTAATGATCGGAGCTTCATCGAGCAGAGCGCAACTTCGCGGATTCGAGTACT 366
DB 284 TGAATGATCGGAGCTTCATGAGAGAGAGAGAAAGTTCGTCAGAGTACTTACT 343
QY 367 GTGCGGCTTCATCTCGCTCCTGAGACGCAACGCGCAGAGAGATCGATGATGAT 426
DB 344 CGAGCAATTTCAATCGCAAGTTCTGATGCTCTGTAAGAGAAATCGGTGCTGAT 403
QY 427 TCTCAAGGTACAGCGTACTATGCTTCAGCTTTCAGCGCGCTTACTCGCTCAACT 486
DB 404 CCTTAAGGTGCAACGGTTTACGAGATTTACGCGGTGACGGCTTACTCTCGCTTA 463
QY 487 TATGATCGGCTTTTGGATTTCTGCGCGGTTGCGGAACAATGGTGGCTCTGCAACT 546
DB 464 TCTGATCGTTTATCATATGCGGTGCGGTCCGCGTGGCAAAATGGGCGCTTGAAC 523
QY 547 TGTATCTGTTGATGCTTGTCTTGGCAGCAAGATGAGAAAGTCTTCTTCACTCT 606
DB 524 CTATCTGTAGCAGCTTGTCTTGTAGCTGCTAAATGAGAGAAACCTTATCTCTAT 583

[illegible][illegible]

Db	511	ACGGCTAATACTTGCTGTGTAACAATCTTCCGATTAGTTTAAAGCAAGTATAAGCTTCACACT	570
OY	524	ACAAGTGGGTGGCCTCGCAMACTTGATNTCTGTGCATGCTTGTCTTGGCAGCAAAGATG	583
Db	571	GATTAAGCATGAGTAGTGTCTAGCGTGTGTGGCTGTCTGTGTCTTAAAGT	630
OY	584	GAGAACCCTTGTGCCATCTCTCTTGAACCTTCAGATAGAAGGTGCCAATACATATT	643
Db	631	GAAAGATTCOAAGTCCATGCTCTTAAGACTCCAAAGTGAAAGAAAGATATCTCTT	690
OY	644	GAGCCGGAACAATTCGTAGATGAGACTACTGTCTCGTGTCTTAAATTTGAGGCTA	703
Db	691	GAAGCTTAAGAGATTCAAAAGAAATGAGACTTTTGATTCCTTACCTTCAATGGAGATG	750
OY	704	AGATCAATACACCACTTGTCTCGCTTCTTGGCTGCAAGATTAATCAACTGA	763
Db	751	CACCTGTGATCCAACTCTTCTTGTGATCACATTATCGCGCATTTGGCTCTAAATG	810
OY	764	ACTTTATCCGTTCTTATTTCCAGGGCAACAGAAATCATGATCTAATATCCAAAG	823
Db	811	CACCAAGCAATTAGCTTCTGTAGGAAGTGGAGCGCTTCTGATCTGTATTTGCTGAT	870
OY	824	GCTAGCTTTCTTGTCTACTGAGCCTTCATGCAATTTGCTGTGACCACTACTGCACT	883
Db	871	ACGAGGTTTATGAGTCACTTCCCTTGCTGTGTAGTACGAAATATGATCTCTGTYTC	930
OY	884	AATGAATTTCTTAATGTGCTGTGTGTAAAGCCGGAATATGCTGAGTCACTGTGCGAGGA	943
Db	931	GAGGAATTAAGCACTGTGATGAATGATTAACAATCTCAATTAACGACTCTACTCAA	990
OY	944	CTAAGAAAAAGAAAGTAATAGGTCCTCTACCACTGTGATCGAAGAGCTTGATTAACAAT	10030
Db	991	GTCATTCAGGAGAAAGTAATGAATGCTATGAAGACTGTGTGTGAGCAATCAACAGCANG	10560
OY	1004	AA 1005	
Db	1051	AA 1052	
RESULT 8			
ID	AAV33886		
DB	AAV33886 standard; cDNA to mRNA; 1431 BP.		
XX	AAV33886;		
AC			
XX			
DT	25-JAN-1999 (first entry)		
XX			
DE	N. tabacum CYCD3;2 gene.		
XX			
KW	D-type cyclin; growth; plant; cell-division control; phosphorylation;		
KM	CDC; Rb; retinoblastoma; germination; flowering; seed; fruit;		
KW	root development; ds.		
XX			
OS	Nicotiana tabacum.		
XX			
PN	WO9842851-A1.		
XX			
PD	01-OCT-1998.		
XX			
PF	24-MAR-1998; 98WO-Ep01701.		
XX			
PR	26-MAR-1997; 97EP-0302096.		
PA	(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.		
PI	Murray JAH;		
XX			
DR	WPI, 1998-532012/45.		
XX			
PT	Regulating growth and structure of plants by modulating protein that		
PT	controls cell division - specifically a D-type cyclin, and related		
PT	chimeric genes and transformed cells and plants, used to alter		
PT	growth rate, flowering, seed production etc.		

XX Claim 14; p55-56; 75pp; English.
PS
XX This sequence represents the CYC3;2 cDNA from *Nicotiana tabacum* which
CC encodes a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin..
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.
XX
SQ Sequence 1431 BP; 387 A; 267 C; 299 G; 478 T; 0 other:

Query Match 5.3%; Score 120.8; DB 19; Length 1431;

Matches 299; Conservative 0; Mismatches 297; Indels 0; Gaps 0;

399 ACGCCAGAGAGATTCAGTTGGATGATTCACAGGTACACGGCTACTATGGCTTTCAGC 458

Db 463 ACCTTAGAAAAGAGCATTGGATTGCATGTTGAGAGTCATTGCTCACATAGGTTTCACTG 522

[illegible]

523 C A G A C T G C T G T T T A C C T G T G A A T A T T T G A T A B G T T G T A T C C G A C A C T C T C C A T C C 502

[illegible]

DV **205** **206**

643 AACCTACAGACACCCCAACCTCCCTTCCTCTTCTAGACCTCCACAGGCGCTGATTCTCAAGATTTTC 702

639 TATTTCAGCCGAGACAAATTCGTAGGATGAGCTACTTGTTCCTCCGCTCTTTAGATTGGA 698

Db 703 TGTTCAGCCAAAGACTATTCAGAGATGCACTCTGGTGCCTCCACTCTTAAGTGGG 762

699 GGCTAGATCAGTAACACCACTTGGCTCCGCGTTCTTGGCGCAAGTAGATTTCA 758

Db 763 AAATGAATCCAGTGACACCACTATCTTTTCATTGATCATATCATGAGAGATTTCGATTC A 822

759 CTGGACTTTTATCCGGTTCCTTATTTCCAGGCAACAGAAATCATCGTATCTAATATCC 818

Db 823 TGACCACTACATTGGATTTCTTAGGAGATGAACGCCCTCAATTCTGGTATTATCA 882

819 AAGAGGCTTCTTCTGCTTACTGGCCCTTCATGCATTGCTGCTGCAAGCCATACACTACAG 8/8

Db 883 CTGATTCAGGCTCTTGCAATTACCTCCACATCTGTATTTCACACTCGAGTAGTAGTATTCG 342

8/9 CAGCTAATGAAATTCCTAATTGGTCGTGGTAAACCCCGAAAATCCTATGATCATTTGCGG 200

||||| ||| | | | ||||

[illegible][illegible]

RESULT 9
RAV33884

XX	
ID	AAV33884 standard; cDNA to mRNA; 1284 BP.

AC AAV33884;
XX

DT 25-JAN-1999 (first entry)
XX

DE N. laudacum circuli gene.
XX

nm D-type cyclin; growing France; coat protein; coat protein; coat protein

Query Match	5.2%	Score 116.8	DB 19	Length 1284
Best Local Similarity	50.7%	Pred. No. 2.8e-19		
Matches 280	Conservative 0	Mismatches 272	Indels 0	Gaps 0
QY 342	ACTTCGTCGGGATTCGAGTACTGTGCGGGTCCCAATCTGCCTCCGAGCCCAAG	401		
DB 405	ACTTTTGGCTTAAGATGATTAATGTCGAGATTTGGAAGTGGAGATTGGATTGAGG	464		
QY 402	CCAGAGAGAAACAGTTGGATGATTTCTCAAGGTACCCGACGATCTATGAGCTTTGACGCTT	461		
DB 465	TGAGAAAGAGAGCTCTTGATTTGATTTTCAAGGCTCATATGACATATGATTTGGAGAGC	524		
QY 462	TGACGGCGGACCTCGCGGCACTATATGATGATGCTTTTGATCTTCGCCGGGTGACGG	521		
DB 525	TGAGTTTTTGTTCGTGATTAATTAATCTTGATGATTTCTATCTGTATGAATTCGCA	584		
QY 522	AAACAATGGGTGCGCTTCGCACTGTATCTGTTGCGATGCTTGTGGCAGCAAA	581		
DB 585	GAAAGTAAACTTGGACAGTGCATTTGTAGCTGTGCGCTGTATACACTTGCAGCCAAA	644		
QY 582	TGGAAGAACCTCTGTTCCATCTCTCTTGAGACCTTCAGATAGAGAGTGCACAGTACATAT	641		
DB 645	TGGAAGAAATTAATGTCTCTTGACTGTGATTAACAGTAGAGGAGTCCAAATTTGTAT	704		
QY 642	TTGAGCGGAGAACAAATCTAGATGAGACTTACTTCTCGGTGCTTATGATTTGAGGC	701		
DB 705	TTGGAAGCAAACTATACAAAGAAAGCACTTTGGTATTAACACATTTGAACTGAGAA	764		
QY 702	TATAGTACATTAACACACTTTGCTGCTGCTCTTTCTTGGTGCAGAGATTTCAAGT	761		
DB 765	TGCAAGCTTATACACTTACATTCATATGATTTATTTATGAGAAAGATGAAATGGATGATC	824		
QY 762	GAACTTTTATCCGGTCTCTTATTTCCAGGCGCAACAGAAATCATGATCTAATATCCAG	821		

Db	825	AAATCCATCTGGCCGCTTGAATTTCTGATCAATGCACTGATATTAAGCATTAATAGAA	888		
Qy	822	AGGCTAGACTTTCTTCTTACTTACGCGCTTCATGCATTTGCTGCGAGCCATTACTCACTGCAG	881		
Db	885	GTAATGATTTCTTTGGAAATTCAGGCTCTCTGAAATATGACAGATCAAGTGGCAATGCTGTTT	944		
Qy	882	CTAATCAAAATTC	893		
Db	945	CAGGGAAATAC	956		
RESULT 10					
ID	AAZ94583	AAZ94583 standard; DNA; 1173 BP.			
XX	AAZ94583;				
DT	18-JUL-2000	(first entry)			
XX	Maize cyclin D ZmCycD gene.				
XX	Maize: cyclin D; ZmCycD gene; CycD: cell division; cell cycle;				
KM	transgenic plant; ss.				
XX	Zea mays.				
OS	MO200017364-A2.				
XX	30-MAR-2000.				
PD	21-SEP-1999,	99WO-US21946.			
XX	23-SEP-1998;	98US-0101551.			
PR	(PION-) PIONEER HI-BRED INP INC.				
PA	Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;				
PI	Hoester GJ;				
XX	WPI: 2000-283589/24.				
DR	P-PADB; AAY79323.				
XX	Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,				
PT	related proteins and antisense RNA useful for control of cell cycle				
PT	regulation				
PS	Claim 1; Page 122-124; 134pp; English.				
XX	The present sequence is that of an isoform of the maize ZmCycD				
CC	gene that encodes cyclin D (CycD, see AAY79323), a protein necessary				
CC	for progression from G1 into S phase. The encoded protein binds to				
CC	CDK4, and the active CycD-CDK4 hyperphosphorylates retinoblastoma				
CC	associated protein, releasing the E2F transcription factor which				
CC	activates DNA synthesis. The invention provides maize CycD				
CC	polynucleotides (see AAZ94581-84) and polypeptides (see AAY79321-24)				
CC	that are involved in cell cycle regulation. Also provided are				
CC	recombinant expression cassettes (including ZmCycD in sense or				
CC	antisense orientation), host cells, transgenic plants (especially				
CC	corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or				
CC	oilseed Brassica) and antibody compositions. A claimed method of				
CC	modulating the level of CycD protein in a cell comprises				
CC	transforming the cell with a recombinant expression cassette				
CC	comprising a CycD polynucleotide linked to a promoter, and				
CC	growing the cell for a time sufficient to induce expression of the				
CC	polynucleotide sufficient to modulate (increase or decrease) the				
CC	CycD protein in the cell. The CycD protein is present in an amount				
CC	sufficient to alter cell division, increase the number of cells				
CC	dividing, improve transformation frequencies, alter plant growth,				
CC	increase the growth rate, increase crop yield, alter plant				
CC	height or size, enhance or inhibit organ (seed, root, shoot, ear,				
CC	tassel, stalk, pollen, stamen) growth, produce organ ablation,				
CC	produce parthenocarpic fruits, produce male sterile plants,				

[illegible]

PR	13-JUL-1999	9905-0143342
PR	14-JUL-1999	9905-01433624
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PR	19-JUL-1999	9905-0144335
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PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match	5.1%;	Score 116;	DB 21;	Length 1356;
Best Local Similarity	52.5%;	Pred. No. 4.6e-19;		
Matches 254; Conservative	0;	Mismatches 230;	Indels 0;	Gaps 0;

[illegible]

DB 846 GAGA 849

RESULT 12
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ID AAC3723 standard; DNA: 1358 BP.
XX AAC3723;
AC
XX 17-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 4087.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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Query Match 5.1%; Score 116; DB 21; Length 1358;
Best Local Similarity 52.5%; Pred. No. 4.6e-19;
Matches 254; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

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OY 405 GAGAGAAATCAAGTGGATGATTCACAGTACACGCGTACTAGCTTTTACGCTTTGA 464
DB 368 GTGAAGAAAGCTCTGATGATGATTTTAAAGTGAATCTCATATAGGTTTATTCATTGA 427
OY 465 CGGCGTACTCGCGCTCAACATATATGATCGGTTTGGATTTCGCCGCGGAA 524
DB 428 CGGCTCTTTAGCTGTATTAATCTCGATAGGTTTATTCACAGCAGAGATTTCAGACAG 487
OY 525 CAATGGGTGGCTCTGCACACTTATCTGTTCATGCTTCTTTGGCACCACAAAGATG 584
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DB 488 ATAGCATGAGATGCTCAGCTTACTGCTTTGGCTGTCTGTCTTTAGCTGCATAGGTTG 547
OY 585 AAGAACCTCTTGTTCATCTCTCTTGAGCCTTCAGATAGAGGTGCCAAGTACATATTTG 644
DB 548 AAGAGATCCGTCTCTCTTCTTCTTATGATTTTCAAGTGAAGAAAGCAATATGCTTTG 607
OY 645 AGCCGAGAACAAATTCGATAGATGAGCTACTTGTCTCGGTGCTTATGATGAGGCTAA 704
DB 608 AAGCTAAGACTATACAGAGATGAGCTTCTGTCTGCTACTGCTGAGAGATGC 667
OY 705 GATCAGTACACACCTTGTCTCTCTCTTCTTGGCTGCAAGTATGATTAAGTCA 764
DB 668 ATCTGTGATCTCAATCTGCTTTTTCATCATATATTCACATACAGCTTTAAATCTC 727
OY 765 CTTTTATCCGGTTCCTTATTTCCAGGCAACAGAAATCATCGATTAATATCCAAAGG 824
DB 728 ATCATCATTTGAGAGTCTTGTGATGATGTAATCTTATTAATCTCATATATCTGAT 787
OY 825 CTAGCTTTCTGCTTACTGCGCTTCATGATGTGTCTGAGGCACTACATGACGCTA 884
DB 788 CGAGATTTCTGAGTTTATGTCCTTCTGTAGCCACTGCACAAATATGCTCTGTTATTA 847
OY 885 ATGA 888
DB 848 GAGA 851

RESULT 13
AAV33889
ID AAV33889 standard; cDNA to mRNA; 1846 BP.
AC AAV33889;
XX 25-JAN-1999. (first entry)
XX
DE Malze CYCD2 gene.
XX
KW D-type cyclin; growth; plant; cell-division control; phosphorylation;
KW Cdc; Rb; retinoblastoma; germination; flowering; seed; fruit;
KW root development; ds.
XX
OS Zea mays.
XX
PN W09842851-A1.
XX
PD 01-OCT-1998.
XX
PE 24-MAR-1998; 98WO-EP01701.
XX
PR 26-MAR-1997; 97EP-0302096.
XX
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX
PI Murray JAH;
XX
DR WPI: 1998-532012/45.
XX
PT Regulating growth and structure of plants by modulating protein that
PT controls cell division - specifically a D-type cyclin, and related
PT chimeric genes and transformed cells and plants, used to alter
PT growth rate, flowering, seed production etc.
XX
PS Claim 14; p64-65; 75pp; English.
XX
CC This sequence represents the CYCD1.1 cDNA from Zea mays which encodes
CC a D-type cyclin. The sequence can be used to alter the growth
CC characteristics or architecture of plants by altering the (functional)
CC level in the plant cells of a cell-division controlling protein that can
CC bind to, or phosphorylate, an Rb-like protein, such as a D-type cyclin.
CC Modulation of the cyclin gene is used to increase or decrease the growth
CC rate, provide faster germination, reduce time to flowering, increase the
CC number of flowers, seeds or fruits per plant, increase root development,
```

CC reduce height and to delay flowering in a range of plants, e.g. legumes,
CC grasses, maize, oilseed rape, wheat, tomato, rice, barley, sunflower,
CC carnation, chrysanthemum, rose, tulip, etc.

XX Sequence 1846 BP; 448 A; 425 C; 514 G; 458 T; 1 other;

Query Match 5.0%; Score 112.2; DB 19; Length 1846;

Best Local Similarity 52.0%; Pred. No. 4.9e-18;

Matches 252; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

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QY 395 GCCAAGCCGAGAGAAATAGTGGATGATTCAGAGGACACGGGCTATAGGCTT 454
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DB 610 GCGCGCCGTGAGAGAGCGCATGATGATGGAGATGGACATTAACAATTTC 669
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 455 CAGCCTTTGACGGGCTACCTCGCCGCAACATATATGATCGGTTTGGATTCTGCGCG 514
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 670 GCACCGTTGACTGCGCTTTGTCTGTACACTGCTGATGATTCCTCCACGATAGAG 729
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 515 TTGCGGGAACAAATGGGTGGCTTCGCAACTGTATCTGTGCAAGCTTCTTTGGCA 574
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DB 730 TTCCCTGAAGGCAAGCTTGGATGATCAGCTCTTGCGAGTGGCGTCTTTGGCT 789
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 575 GCAAAAGATGGAAGAACTCTTGTTCATCTCTTGGACCTTCAGATGAAAGTGCCAG 634
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DB 790 TCGAAATCGAAGAGACTTTTGTGCCACTCCCTTGGATTGGACGAGCGAGGCAAG 849
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QY 635 TACATATTTGAGCGAGAAATCGATGATGAGACTTGTCTCGGTCTTAGAT 694
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DB 850 TTTGTTTGGGAGAGACATATAAAGATGAGCTCTGCTGCTAAGACCTTAAG 909
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QY 695 TGGAGGCTAAGATGATTAACACCACTTGTCTCGCTTCTTGGCTGCAAGTAGAT 754
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DB 910 TGGAGGATGATGCTGTTACTGCTTGCATTTGTGAATCTTCTCAATAATGAGT 969
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QY 755 TCAACTGGAATTTATCCGCTTCCTTATTTCCAGGAGCAAGAAATCATGTAAT 814
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 875 ACTGC 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1090 GCTGC 1094
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 14
AAZ94581
ID AAZ94581 standard; DNA; 1861 BP.

XX AAZ94581;

XX 18-JUL-2000 (first entry)

XX Maize cyclin D ZmCycd gene.

XX Maize; cyclin D; ZmCycd gene; Cycd; cell division; cell cycle;

XX transgenic plant; ss.

XX Zea mays.

XX Key Location/Qualifiers

XX FT 275..1351

XX CDS /*tag= a

XX WO200017364-A2.

XX 30-MAR-2000.

XX 21-SEP-1999; 99WO-US21946.

XX 23-SEP-1998; 98US-0101551.

XX (PION-) PIONEER HI-BRED INT INC.

XX Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;

XX Hoerster GJ;

XX WPI: 2000-283589/24.

XX P-PSDB: AAY9321.

XX Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,

XX related proteins and antisense RNA useful for control of cell cycle

XX regulation -

XX Claim 1; Page 115-117; 134pp; English.

The present sequence is that of an isoform of the maize ZmCycd gene that encodes cyclin D (Cycd, see AAY9321), a protein necessary for progression from G1 into S phase. The encoded protein binds to CDK4, and the active Cycd-CDK4 hyperphosphorylates retinoblastoma associated protein, releasing the E2F transcription factor which activates DNA synthesis. The invention provides maize Cycd polynucleotides (see AAZ94581-84) and polypeptides (see AAY9321-24) that are involved in cell cycle regulation. Also provided are recombinant expression cassettes (including ZmCycd in sense or antisense orientation), host cells, transgenic plants (especially corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or oilseed Brassica) and antibody compositions. A claimed method of modulating the level of Cycd protein in a cell comprises transforming the cell with a recombinant expression cassette comprising a Cycd polynucleotide linked to a promoter, and growing the cell for a time sufficient to induce expression of the polynucleotide sufficient to modulate (increase or decrease) the Cycd protein in the cell. The Cycd protein is present in an amount sufficient to alter cell division, increase the number of cells dividing, improve transformation frequencies, alter cell growth, increase the growth rate, increase crop yield, alter plant height or size, enhance or inhibit organ (seed, root, shoot, ear, tassel, stalk, pollen, stamen) growth, produce organ ablation, produce parthenocarpic fruits, produce male sterile plants, enhance embryogenic response, increase callus induction, provide positive selection, increase plant regeneration, alter the time that cells are arrested in G1 or G0 phase or in a particular cell cycle, improve response to environmental stress including dehydration, heat or cold, increase the number of pods per plant, increase the number of seeds per pod or ear, alter the lag time in seed development, provide hormone-independent cell growth, or increase the growth rate of cells in bioreactors. The level of Cycd protein in the cells is transiently modulated by introducing Cycd RNA or Cycd polypeptides. Cycd polynucleotides can be used to identify Cycd interacting proteins. All claimed.

XX Sequence 1861 BP; 462 A; 413 C; 512 G; 474 T; 0 other;

Query Match 5.0%; Score 112.2; DB 21; Length 1861;

Best Local Similarity 52.0%; Pred. No. 4.9e-18;

Matches 252; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

```

QY 395 GCCAAGCCGAGAGAAATAGTGGATGATTCAGAGGACACGGGCTATAGGCTT 454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 569 GCGCGCCGTGAGAGAGCGCATGATGATGGAGATGGACATTAACAATTTC 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 455 CAGCCTTTGACGGGCTACCTCGCCGCAACATATATGATCGGTTTGGATTCTGCGCG 514
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 629 GCACCGTTGACTGCGCTTTGTCTGTGAATCTGATGATGATTCCTCCACGATAG 688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 515 TTGCGGGAACAAATGGGTGGCTTCGCAACTGTATCTGTGCAAGCTTCTTTGGCA 574
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 689 TTCCCTGAAGGCAAGCTTGGATGATCAGCTCTTGCAAGTGGCTGTCTTTGGCT 748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 575 GCAAAAGATGGAAGAACTTGTTCATCTCTTGGACCTTCAGATGAAAGTGCCAG 634
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 749 TCGAAATCGAAGAGACTTTTGTGCCACTCCCTTGGATTGGACGATAGCGGCAAG 808
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 22:41:35 ; Search time 2663 Seconds

(without alignments)
11449.351 Million cell updates/sec

Title: US-09-665-308D-11

Perfect score: 2259

Sequence: 1 acaacttcctccatcctc.....ttaaaaaaaaaaaaaaaaaa 2259

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_estum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inu:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	525.8	23.3	548	10	B1427409
2	518	22.9	560	10	B1785106
3	508.6	22.5	809	10	BG585146
4	492.2	21.8	834	10	BG585934
5	489.4	21.7	810	10	BG646052
6	483.4	21.4	775	10	BG645553
7	450.8	20.0	663	10	B1770081
8	429.4	19.0	480	10	BG238202
9	408.2	18.1	533	10	BG238135
10	406.8	18.0	718	10	BG647122
11	382.8	16.9	749	10	BG886881
12	337.2	14.9	621	10	B1432702
13	329	14.6	558	10	BG520221
14	310.6	13.7	716	10	BG526521
15	287	12.7	728	10	BG597062
16	229.8	10.2	313	10	BFO08678
17	215	9.5	651	9	AW776661

18	211.2	9.3	658	9	AM981189
19	205.6	9.1	501	10	B1436332
20	169.8	7.5	585	10	BG595067
21	169.6	7.5	515	10	BE323695
22	166	7.3	287	10	BE801432
23	149	6.6	197	10	BF636916
24	145.6	6.4	557	10	BK309337
25	142	6.3	583	9	A1812774
26	141	6.2	813	9	BE642779
27	134.8	5.9	546	9	AM944884
28	132.8	5.9	478	10	BE472260
29	129.4	5.7	596	9	AM042725
30	129.2	5.7	659	10	BK358501
31	127.2	5.6	523	10	BE472243
32	126.6	5.6	731	10	BM408328
33	126.6	5.6	802	10	B1207010
34	125	5.5	666	10	B1210187
35	118	5.2	621	10	BE442681
36	113.6	5.0	485	10	BG132909
37	113.2	5.0	790	10	B1306295
38	112.2	5.0	558	9	AM036252
39	109	4.8	608	9	AM735876
40	108.8	4.8	478	9	AV527915
41	107	4.7	516	10	B1211043
42	105.4	4.7	546	10	B1204893
43	105.4	4.7	725	10	B1203937
44	105.4	4.7	727	10	B1204715
45	105.4	4.7	727	10	B1205090

ALIGNMENTS

RESULT 1
B1427409
LOCUS
DEFINITION
ID: Gm-c1049-4594 5', mRNA sequence.
ACCESSION
B1427409
VERSION
B1427409.1 GI:15204641
KEYWORDS
SOURCE
ORGANISM
soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 548)
Shoemaker,R., Keim,P., Vodkin,L., Eprelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Rutter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1993)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccutresgen.com
High quality sequence stop: 421.
Location/Qualifiers
1..548
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1049-4594"
/clone_1lb="Gm-c1049"

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/tissue.type="whole seedlings of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
/Note="Vector: pBluescript II SK+, Site_1: EcoRI; Site_2:
XhoI; The Clark NII, was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 3 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."
BASE COUNT      167 a      70 c      150 g      161 t
ORIGIN
Query Match      23.3%; Score 525.8; DB 10; Length 548;
Best Local Similarity 98.5%; Pred. No. 4.5e-75;
Matches 541; Conservative 0; Mismatches 7; Indels 1; Gaps 1;
QY 1424 TGCAGATTCCACCTAGGAGAGGATTTTGCACATGTTACCGTGGAGAGAAATGAG 1483
DB 1 TGCAGATTCCACCTAGGAGAGGATTTTGCACATGTTACCGTGGAGAGAAATGAG 60
QY 1484 AGAAGAAAGATGAAACACTGAAACGAGGATGAGAAATTTAATGATTTCTTCTGT 1543
DB 61 AGAAGAAAGATGAAACACTGAAACGAGGATGAGAAATTTAATGATTTCTTCTGT 120
QY 1544 AACCTGATTCCTGAGAGAGAAATGATTTGGGGCTGATTTCAAGTTTGCATTAA 1603
DB 121 AACCTGATTCCTGAGAGAGAAATGATTTGGGGCTGATTTCAAGTTTGCATTAA 180
QY 1604 TACTTGGTGAAGAGATGAAAGATGTTGGGGCAACGCTGTAGAGATTGAGAGAGAAA 1663
DB 181 TA-TTGGTGAAGAGATGAAAGATGTTGGGGCAACGCTGTAGAGATTGAGAGAGAAA 239
QY 1664 AAGTAGAGAGAAAGATGAAAGATGTTGGGGCAACGCTGTAGAGATTGAGAGAG 1723
DB 240 AAGTAGAGAGAAAGATGAAAGATGTTGGGGCAACGCTGTAGAGATTGAGAGAG 299
QY 1724 AAGTGTCAATGTCATATCATCTGATTCATTAAGCAAGCAAGCTGATTTTGGCCA 1783
DB 300 AAGTGTCAATGTCATATCATCTGATTCATTAAGCAAGCAAGCTGATTTTGGCCA 359
QY 1784 GCATCAGTCTTCTCATCATCCAGTACTACTACTTGTATGGAGCCCTCAACAGTAA 1843
DB 360 GCATCAGTCTTCTCATCATCCAGTACTACTACTTGTATGGAGCCCTCAACAGTAA 419
QY 1844 GAAACATTTGAAGGCAATTAAGTTTGGCTACAAATGCTGGACTTTTGTGGG 1903
DB 420 GAAACATTTGAAGGCAATTAAGTTTGGCTACAAATGCTGGACTTTTGTGGG 479
QY 1904 TATTGGCAGCTGTGCACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1963
DB 480 TATTGGCAGCTGTGCACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
QY 1964 CTTTTCCTT 1972
DB 540 CTTTTCCTT 548
RESULT 2
BI785106      560 bp      mRNA      linear      EST 30-NOV-2001
LOCUS      BI785106      sat37a11.y1 Gm-cl065 glycine max cDNA clone GENOME SYSTEMS CLONE
DEFINITION      ID: Gm-cl065-5397 5' similar to SW:GCD1_ARATH P42751 CYCLIN
DELTA-1. ;, mRNA sequence.
ACCESSION      BI785106

```

```

VERSION      BI785106.1 GI:15812831
KEYWORDS      EST.
SOURCE      soybean.
ORGANISM      Glycine max
REFERENCE      1 (bases 1 to 560)
AUTHORS      Shoemaker R., Keim P., Vodkin L., Erpelting J., Corryell V., Rhanna
A., Bolla B., Marra M., Hillier L., Kucaba T., Martin J., Beck C.,
Wyllie T., Underwood R., Steptoe M., Theising B., Allen M., Bowers
Y., Person B., Swaller T., Gibbons M., Pape D., Harvey N., Schurk
R., Ralster E., Kohn S., Shin T., Jackson Y., Cardenas M., McCann
R., Waterson R. and Wilson R.
Public Soybean EST Project
TITLE      Unpublished (1999)
JOURNAL      Contact: Shoemaker R./Public Soybean EST Project
COMMENT      Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cou@resgen.com
Seq primer: -40RP from Gldco
High quality sequence stop: 422.
location/Qualifiers
1. 560
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl065-5397"
/clone_1db="Gm-cl065"
/tissue_type="germinating shoots"
/lab_host="DH10B"
/Note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
germinating shoots of the cultivar Williams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a blunt-ended cDNA fragments
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
Shoemaker."
BASE COUNT      108 a      180 c      137 g      135 t
ORIGIN
Query Match      22.9%; Score 518; DB 10; Length 560;
Best Local Similarity 96.3%; Pred. No. 8e-74;
Matches 543; Conservative 0; Mismatches 15; Indels 6; Gaps 1;
QY 26 CAACACACACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 85
DB 3 CATCAACAACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 62
QY 86 GGTGAGGTTCCGGCAACCTCATCGGCAATCGGCAATGCGACATGATGATGGAACCT 145
DB 63 GGTGAGGTTCCGGCAACCTCATCGGCAATCGGCAATGCGACATGATGATGGAACCT 121
QY 146 CCGCTGCCGCGCGCGCTCTCATGTGCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 205
DB 122 -----ACGCGCGGGGGTCTCTCATGTCGCTGCTCTCTCTCTCTCTCTCTCTCTCT 176
QY 206 GCGGAGAGCTCTCTCGGAATCTCTCTCGGAGATGCGCGGAGATGCTCTCTCTCTCTCT 265
DB 177 GCGGAGAGCTCTCTCGGAATCTCTCTCGGAGATGCGCGGAGATGCTCTCTCTCTCTCT 236

```


Oy	266	GACCTCCTAACCCCTCCGCGCGTGGCGAGAGAAAGATTGTTATTCGATCCGAGGCTTC	325
Db	237	GACTCTCTACCTCCCTCCGCCCGTCCGCGAGACAGAGAGATTGTTATTCGATCCGAGGCTTC	296
Oy	336	ATCGAGCAGAGAGCGCACTTGTTCCGGGATTTCGAGTACCTGTCCGGGTTCCAAATCTCGC	385
Db	297	ATCGAGCAGAGAGCGCACTTGTTCCGGGATTTCGAGTACCTGTCCGGGTTCCAAATCTCGC	356
Oy	386	TCCCTGAGACGCCAAGCCAGAGAAATACAGTTGGATGGATCTCAAGTACACCGGTAC	445
Db	357	TCCCTGAGACGCCAAGCCAGAGAAATACAGTTGGATGGATCTCAAGTACACCGGTAC	416
Oy	446	TATGCTTTACGCTTTTGACGGCGTACCTCGCGCTCAACTATATGATGCGCTTTTGGAT	505
Db	417	TATGCTTTACGCTTTTGACGGCGTACCTCGCGCTCAACTATATGATGCGCTTTTGGAT	476
Oy	506	TCTCCCGGTTCCCGGAAACAATAGGTGGGCTCTGCAACTGTATCTGTTCATGCTTG	565
Db	477	TCTCCCGGTTCCCGGAAACAATAGGTGGGCTCTGCAACTGTATCTGTTCATGCTTG	536
Oy	566	TCTTTGGCAGCAAAAGATGGAAGA	589
Db	537	TCTTTGGCAGCAAAAGATGGAAGA	560

RESULT 3	
LOCUS	BG585146
DEFINITION	BG585146 809 bp mRNA linear EST 11-APR-2001 EST4486909 MHAM Medicago truncatula/Gloms versifidme mixed EST library cDNA clone pMHAM-22A23 5' end, mRNA sequence.
ACCESSION	BC055146

accession BG562140
 version BG562146.1 GI:13600210
 keywords EST.
 source Medicago truncatula/Glomsus versiforme mixed EST library.
 organism Medicago truncatula/Glomsus versiforme mixed Est library
 Eukaryota, mixed EST libraries.

REFERENCE AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 809) Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Uteerback,T., Cho,J. and Fraser,C.M.	Ests from roots of <i>Medicago truncatula</i> after colonization with <i>Glomus versiforme</i> , 2001	Unpublished (2001)	Contact: Harrison M.J.

Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mharrison@noble.org
Noble EST name: N380619e Y1GR sequence name: MTDC412TK More
information is available at: <http://www.medicalgo.org>
Seq primer: Skmdd (CTA gAA cTg gAT gAT CC).

FEATURES	Location/Qualifiers
SOURCE	1. .809

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/organism="Medicago truncatula/Glomsus versiforme mixed EST
library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-22A23"
/clone_lib="MHAM"
/lisue_type="roots colonized with Glomsus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomsus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XL0LR"
/notes="Vector: plasmidscript SR-1; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomsus versiforme. The cDNA was
directionally ligated into the unique XR vector from
Stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised

```

BASE COUNT	194 a	196 c	173 g	246 t
ORIGIN	from the recombinant lambda-zap phage using Ex-3ass15 helper phage and propagated in K10LR cells."			

Query Match	22.5%	Score 508.6	DB 10	Length 809
Best Local Similarity	78.7%	Pred. No. 2.3e-72		
Matches 637; Conservative	0	Mismatches 159	Indels 13	Gaps 2

Oy 158 GCGGCTCATGTGGCTTTCCTCCGCTCTCCGACTACGAGCCTCTCTGCGGAGGACTCC 217
||| ||||| | ||| ||| ||||| ||| ||||| ||| |||||
Db 1 GCATTTCTCAAGCCACATCTCCAGCACCTCCGAGCTGCTCTGCGGGAGGACTCG 60

Qy 218 TCCGGAATCCTCTCCGGAGAGTCGCCGGAGTGTCTCTTCTCCGACATCGACTTCCTCACT 277
 ||| | ||||| ||||| | ||||| ||||| | ||||| |
 Db 61 TCCGAGCTCCCTCACCCGGAGATTACCCGAGATGCTCTCCGACCTGGATTTCATCATCATCA 120

```

Oy 278 CCTCCGCCGTCGCCGACACA-----GAGATTGTATTTCGATCCGAGCTTC 325
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 TCGCAGTTGCCGTCGTCGTCATTATTGCCGAGGAGAGAGAGAGATTCCTGTTTTC 180

```

Qy 326 ATGAGCAGCAGGCAACTTCGTTCCGGGATTGCACTACCGTCCGGGTTCCAATCTCGC 385
|||||
Db 181 ATGAGCAGCAGGTTCAAGTTGTTCCTGGTTTCAGCTACGCTCTCAAGATTCGAATCTCGC 240

Qy 386 TCCCTGACGCCAACGCAGAGAAGAAATCAGTTGGATGGATTCTCAAGGTACACGCGTAC 445
|| || | ||| | ||||| || | ||| ||||| ||||| |||
Db 241 TCTCTCGAATCCAGCACACCAGAGAAGAACCATTCGATGATGATCTCTCAAGGTACATGAGTAT 3000

QY 446 TATGGCTTTCAGCCTTTGACGGCGTACCTCGCCGTCAACTATATGATCGGTTTTGGAT 505
||||| ||||| || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TATGGAATTTCAGCCGTTAACGGCGTACCCTCTCCGTTAACTATATGATCGGTTTTGGAT 366

QY 506 TCTGCGGGTTGCCGAACAATGGGTGGCCTTCGCACTTGTATCTGTCATGCCTTG 565
||||| - || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 TCTGCACCTTACCAGGATCAAATGAGAGCCACTGCACACTTTACTGTTGCATGTTTG 420

QY 566 TCTTGGCAGCAAGATGGAGAACCCTTGTTCATCTCTCTTGACCTTCAGATGAA 6225
||||| ||||||| ||||||| ||||| ||| ||||||| |||
Db 421 TCTTTACGACGAAGATGGAGGACCACTGGTTCCTTCTTACCTTTAGACTTTGAGAA 4880

QY 626 GGTGCCAGTACATATTGAGCCGAGAACATTCCTAGATGGAGCTACTTGTCTCGGT 6839

Db 481 GGTGCCAAATCATATTTCACACAGGAGCATTCCTAGAAATGGAGCTGCTTCTCTCACT 5408

DQ 686 GTCTTAGATTGGACGCGTTAAGATCAGTAACACCACCTTGTGCCTTCGCTTCTTTGGCGCC 745
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 541 ATTTTGGAATGGAGGCGAGATCAATACCCCACACTAGTTTCCCTCACTTTCTTTGGCGCGC 600

QY 746 AAGTAGATTCACTGGAACTTTTATCCGGTTCCTATTTCAGGSCACAGAAATCATC 8059
|| |||||
Db 601 AAGCTGGATTCACTGGAACTTTTATCCGGTTCCTATTTCAGGSCACAGAAATCATC 6600
|| |||||

OY 806 GATCTAATATCCAGAGGCTTCTTCGTACTGGCCTTCATGCATTGCTGCTCCA 8655
| | | | | | | | | | | | | | | | | | | | | |
Db 661 TTATCTCAATATCCAGAGTGCTAGCTTTCTTAACTTAACAGGCCCATCATCATATTCGCTGCGCCT 720

QY 866 GCCATACCTACTGACAGCTAATGAATTCCCTAATTGGTCTGTGGTTAAGCCCAAAATGCT 925
||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 721 GCCATACCTCTCGCAGCTAATGAATAATTCCTTAATGGTCTGTGGTTAAATGCCTAACCTAATGCT 780

OY 926 GAGTCAT-GGTGCGAGGACTAAGAAMG 953
 || ||||| |||| | ||||| ||||
DH 781 GAATCATGGCTMGCAACGACTAACCAAAG 808

RESULT 4
DCE0503A

LOCUS	834 bp	mRNA	linear	EST 11-APR-2001
DEFINITION	EST1487699	MHAM Medicago truncatula/Clonmms versiforme mixed EST		
ACCESSION	Library cDNA clone PMHAM-31L19 5' end, mRNA sequence.			
VERSION	BG585934.1	GI:13600998		

KEYWORDS	EST
SOURCE	Medicago truncatula/Glommus versiforme mixed EST library.
ORGANISM	Medicago truncatula/Glommus versiforme mixed EST library.
REFERENCE	Eukaryota, mixed EST libraries.
AUTHORS	1 (bases 1 to 834)
TITLE	Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Uterback,T., Cho,J. and Fraser,C.M.
JOURNAL	ESTs from roots of Medicago truncatula after colonization with Glommus versiforme, 2001
COMMENT	Unpublished (2001) Contact: Harrison M.J.

BASE COUNT	198 a	205 c	176 g	255 t
ORIGIN				

Query Match	21.8%;	Score 492.2;	DB 10;	Length 834;
Best Local Similarity	77.1%;	Pred. No. 9.9e-70;		
Matches 645;	Conservative 0;	Mismatches 173;	Indels 19;	Gaps 3

Oy	103	CTATCGGGGATATGGCAATGCAACACAAATGAATGGGAGAACTCCGCGCGCGCGCT	162
Db	4	CTCTGTGGATCTAACACATGACACAAAGCAATGATTGAAG-----GCAATTCGCGCAAT	57
Oy	163	CTCTATGTCGGTTCCTCGCTCTCCGACTACGACCTCCCTGCGGAGAGACTCCCTCGG	222
Db	58	TCTCATGCCACATCTGTCCAGACACTCCGACATCGCAGCTCTCTCGCGGAGAGACTCTGTGGA	117
Oy	223	AATCTCTCCGGAGAGTCGCGGAGTGGCTCTCTTCGCAATCGACTCTCACTTCCTCC	282
Db	118	GGTCTCAACCGGAGATTATACCGAATGGCTCTCCGACCTGGATTCATCATTCATTCACGGA	177
Oy	283	GCCGTTCGCCGACGACA-----GAGCATTTGTTATTGATCGCAGCTTCATCGA	330
Db	178	GTTGGCCGTCTGTCGATTATTATTCGCGAGGAMGAGGAGTGAGTATGCTGTTTTCATCGA	237
Oy	331	GCACAGCGGCACATTCGTTCGCGGATTCGAGTACCTGTGGCGGTTCCAAATTCGCTCCCT	390
Db	238	GCACAGATTCAGTTGTTGTCCTCGGTTTCGACATACGCTCATAATTCACATTCCTGCTCTCT	297
Oy	391	GGAGCGCAACGCGAGAGAAGATCAGTTGGATGGAGANTCTCAAGGTCACGCGTACTATGG	450
Db	298	CGAATTCGACACCAAGAGAAGCCATATTCATGAGATTCACAAGATACATGAGATATTAATG	357

Oy	451	CTTTCAGCCTTTGAGCGGCTACCTCGCCGCTACATCATATGATGGCTTTTGATCTCG	510
Db	358	ATTTCAGCCGTTAACGGGGTACCTTCGCTTAACTATATGATGGCTTTTGATCTCG	417
Oy	511	CCGTTTGGCCGGAAACAATATGGGTGGCTCTCTCAACTTATCTGTGATCCTGTCTT	570
Db	418	ACCTTTACCGGATCAATATGATGGCCACCTGCACACTTTATCTGTGGATCTTTGTCTT	477
Oy	571	GGCAGCAAAAGATGGAGAACTCTTGTTCATCTCTCTTGGACCTTCAGATAGAGTGC	630
Db	478	AGCAGCAAAAGATGGAGGAACCACTGGTTCCTCTCTCTTCAACTTCAGATTGAAGTGC	537
Oy	631	CAAGTACATATTTTGGCCGAGCAACATCTGATGATGGAGTACTTGTATCTCGGGTCTT	690
Db	538	CAATATCATTTTTCACCAAGAGACATCTTATGATATGAGCTGTGTCTGCACATTTT	597
Oy	691	AGATTGAGGCTAGATCATATACACCACTTGTCTCTCGCTTCTTTCGCTGCAAAAGT	750
Db	598	GGATTGGAGGCTGATGATCAATCACCCCACTAGTTTCTTCAGTTTCTTGGGTGCAAGCT	657
Oy	751	AGATTCACCTGGAACCTTATTCGGTGTCTTATTTCCAGGGCAACAGAAATCATGCTATC	810
Db	658	AGATTCACCTGGAACCTTACCCCACTTATATTTTACAGCTGTACAGAAATCATCTTATTC	717
Oy	811	TAAATATCCAAAGAGCTAGCTTTCCTTGGCTTACTGGCCCTTATGACATTTGCTGTGACCCAT	870
Db	718	TAAATATCCAAAGAGCTAGCTTTCCTTACTTACAGGCGCATCATGCAATTGTGAGCGTCAT	777
Oy	871	ACTGACTGACGATATGAAATTCCTAATT-GCTGTGGTATAGGCCCAAAATGTGTG	926
Db	778	ACTGCTCTGACGATATGAAATTCCTAATTTGGCTTGTGTATATTCCTAGAGCATGTGTG	834

[illegible]

REFERENCE	1 (bases 1 to 810)
AUTHORS	Vandenbosch K., Endre, G., Hur, J., Beremand, P., Town, C.D., Bowman, C.L., Craven, M.B., Chu, J. and Fraser, C.M.
TITLE	ESTs from roots of <i>Medicago truncatula</i> 72 h after Rhizobium inoculation, 2001
JOURNAL	Unpublished (2001)
COMMENT	Contact: Vandenbosch K Department of Biology Texas A&M University College Station, TX 77843-3258, USA Tel: 409 845 7707 Fax: 409 845 2891 Email: kate@mail.bio.tamu.edu M3344596 TIGR sequence name: MTECU45TK More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gTg gAT CC), Location/Qualifiers 1..810
FEATURES	
SOURCE	

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/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:380"
/clone="PKV3-48G20"
/clone_1id="KV3"
/tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
meliloti"

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QY 472 CTTGCGGCTCACTATATGATGCGTTTGGATTCTCGCCGGTCCGGAAACAATGC 531
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Db 301 CCTCTCGTTAACTATATGATGCGTTTGGATTCTCGACCTTACCGAATCAAAATG 360
QY 532 GTGGCCCTGCAACTGTTATCTGTGATGCTGTTGCGTGGCAGCAAGATGGAAGACC 591
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 ATGGCCACTGCAACTGTTATCTGTGATGCTGTTGCGTGGCAGCAAGATGGAAGACC 420
QY 592 TCTGTTCATATCTCTTGGACCTTGCAGATGAGAGTGCACAAATATTTGGACCGAG 651
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 ACTGCTTCCTCTCTCTTGAAGCTTTCAGATTTGAAGTCCCAATACATATTTCAACCAAG 480
QY 652 AACAAATCGAGATGAGAGTACTTGTCTCGTCTTACATTTGAGAGGCTAAGATCAGT 711
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 GACATTTCTTGAATGAGAGTCTTGTCTGACTATTTTGGATTTGAGAGGCTGAGATCAAT 540
QY 712 AACACCACTTGTCTCTCGTCTTGTCTTGCAGCAAGATGATTTCACTGCACTTTTAT 771
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 CACCCCACTTGTCTCTCGTCTTGTCTTGCAGCAAGATGATTTCACTGCACTTTTAC 600
QY 772 CCGGTTCTTATTTCCAGGCGACAGAAATGATGATATATATCCAAAGAGGCTAGCTT 831
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 CCACTTATATATTTACGCTGCTACAGAAATCATCTTATATATCCAAAGATGCTAGCTT 660
QY 832 TCTGTCTTACGCGCTTCACTGATTTGCTGTCAGACCATCACTCACTGAGCTAATGAAT 891
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 TCTTACTTACAGGCGATCATGATTCGTCAGAGTGGCCATCTCTCTGAGCTAATGAAT 720
QY 892 TCTTATTTGCTCTGTGTTAAGCCGAAATGCTGATGATCG 934
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Db 721 TCTTATTTGCTCTGTGTTAAGCCGAAATGCTGATGATCG 763

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RESULT 7
BI270081 663 bp mRNA linear EST 18-JUL-2001
LOCUS NF004A12PLF1097 Developing flower Medicago truncatula cDNA clone
DEFINITION
BI270081.1 GI:14877355
VERSION
BI270081.1 GI:14877355
KEYWORDS
SOURCE
ORGANISM
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE
1 (bases 1 to 663)
AUTHORS
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Iman, J.T., Weller, J.W. and May, G.D.
TITLE
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula flower library
JOURNAL
Unpublished (2001)
COMMENT
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 663 Std Error: 0.00
Plate: 004 Row: A Column: 12
Seq primer: TCACACAGAAACAGCTATGAC.
FEATURES
SOURCE
1..663
Location/Qualifiers
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF004A12PL"
/clone_lib="Developing flower"
/tissue_type="Developing flowers"
/der_stage="Developing pooled, Contains a mixture of
very young, developing, fully-opened flowers and flowers

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in early transition into pods."

/note="Vector: Lambda Zap; cDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-opened flowers and flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Gold packaging extracts. Phagemids containing Uni-Zap XR vector in vivo excised from the recombinant Uni-Zap XR vector using Exsist helper phage and the E. coli strain XL1-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."

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BASE COUNT      181 a      148 c      136 g      198 t
ORIGIN
Query Match      20.0%; Score 450.8; DB 10; Length 663;
Best Local Similarity 81.6%; Pred. No. 4,86-63;
Matches 550; Conservative 0; Mismatches 112; Indels 12; Gaps 2;

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QY 482 AACTATATGATCGGTTTGGATTCTGCGGTTCCGGAACAATGSGTGGCTCTG 541
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Db 2 AACATATGATCGGTTCTGTAATCTCGGGGTGCGCAACAATAGGTGGCCACTG 61
QY 542 CAACCTGATCTGTTCATGCTCTCTTGGCAGCAAGATGGAAGAACTCTGTGCCA 601
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 CAACCTTCTATGATGCTCTCTTGTCTTGTACCTGCAAAAGATGGAAGAACTTGTCTCT 121
QY 602 TCTCTTGGACCTTCAGATGAAAGTGCAGATATTTGAGCCGAGAAATTTGCT 661
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 TCTCTATTTGACCTTCAGATGAAAGTGTCAAAATACATGTTGAACCCATTAATTTGA 181
QY 662 AGGATGAGCTAATCTGTTCTGCGTCTTGAATTTGAGGCTTAAGATCACTAACCACTT 721
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 AGAATGAGAGCTAATCTGTTCTTAAATGTTGATGAGGCTTAAGATCACTAACCACTT 241
QY 722 TGTCTCTGCTCTTCTTCTTGGCAGAAATGATTTCACTGGAACCTTTATCTGCTT 781
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 AGCTTCTCAGATTTCTTGGCGGAAATGATTAACCTTCACTTACTGCGTTCTC 301
QY 782 ATTTCAGGCGAAGAAATCATGATCTATATTCAGAGAGGCTTCTTCTTAC 841
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 ATTTCAGAGCTTACACAAATTTATCTTATTTCAATTCAGAGGCGAAGCTTCTTCTAT 361
QY 842 TGGCCTTCACTGATGCTGCTGCTGACCCATCTCACTGAGCTAATGAATTTCTTATTTG 901
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 TGGCCTTCACTGATGCTGCTGACCCGCTATACCTATGACGTAAGAAATTTCTTATTTG 421
QY 902 TCTGTGTTAAGCCGAAATGCTGATGCTGCGAGGAGCTAAGAAAGAAAGTA 961
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 TCTGTGTTAAGCCGAAATGCTGATGCTGCGAGGAGCTTAAAGAAAGAAATTT 481
QY 962 ATAGGCTGTACAGTTGATGCAAGAGCTTGTGATTAACAAATACCAAGAAATCTCCC 1021
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Db 482 ATAGGCTGTACAGTTGATGCAAGAGCTTGTGATTAACAAATACCAAGAAAGAAATCTCCC 540
QY 1022 TTACTAAAGATGTTGGCCGAGCTGCGAGTAACACTGCGAGCCGAGTCAAGTACT 1081
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 -----TAAAGTTTGGCAAAATGCGAGTGAACATTCAGCCCTTATGAGTCAATGTGC 595
QY 1082 GTATCATCTTCTCATCTCTTCAACCTCTCTCTCTCTCTTGTAAAGAGAGAAA 1141
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 596 TGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 649
QY 1142 TTAATTAACCGTTT 1155
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Db 650 TTAATTAACCGTTT 663

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RESULT 8
BG238202 480 bp mRNA linear EST 28-NOV-2001
LOCUS BG238202
DEFINITION
Bg238202 y1 Gm-c1043 glycine max cDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1043-4046 5' similar to SM:CGD1_ARAHN P42751 CYCLIN

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DELTA-1.1, mRNA sequence.

ACCESSION BG238202
 VERSION BG238202.1 GI:12773275
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 480)
 Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kueba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Rheising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gidbons,M., Pape,D., Harvey,N., Schurk,R., Rilter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished (1999)

TITLE Public Soybean EST Project
 JOURNAL Contact: Shoemaker R/Public Soybean EST Project
 COMMENT Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccul@resgen.com
 High quality sequence stop: 445.

FEATURES
 source
 1..480
 Location/Qualifiers
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1043-4046"
 /clone_1lb="Gm-c1043"
 /tissue.type="Hypocotyl and Plumule, germinating seeds"
 /lab.host="DH10B"
 /note="Vector: pT73pac (Pharmacia); Site_1: EcoRI; Site_2: NotI; This cDNA library was constructed from mRNA isolated from hypocotyl and plumule tissues of seeds germinated for three days of the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and NotI. The cDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the pT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 89 a 164 c 112 g 115 t

ORIGIN

Query Match 19.0%; Score 429.4; DB 10; Length 480;
 Best Local Similarity 95.4%; Pred. No. 1.5e-59;
 Matches 455; Conservative 0; Mismatches 16; Indels 6; Gaps 1;

26 CAACACACACACTCTCTCCCTCTCTGACACCAAAACCACTTCGCGGACATCTCC 85
 11 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 10 CACACACACACACTCTCTCTCCCTCTCTGACACCAAAACCACTTCGCGGACATCTCC 69
 86 GGTCCAGTTCGGGACCTCATGTCGGGATTCGGGATTCGGGATTCGGGATTCGGGATTC 145
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 70 GGTCCAGTTCGGGACCTCATGTCGGGATTCGGGATTCGGGATTCGGGATTCGGGATTC 128
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 146 CCGGTCCAGTTCGGGACCTCATGTCGGGATTCGGGATTCGGGATTCGGGATTCGGGATTC 205
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 129 -----ACGCGCGGGGCTCCATGTCGGGATTCGGGATTCGGGATTCGGGATTCGGGATTC 183
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 206 GCGGAGACTCTCTCCGATCTCTCCGAGATTCGGGATTCGGGATTCGGGATTCGGGATTC 265
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 184 GCGGAGACTCTCTCCGATCTCTCCGAGATTCGGGATTCGGGATTCGGGATTCGGGATTC 243

266 GACTCTCTACCTCTCTCCGCGCTCCGCGGACGACGACGATTTGATTCATCCGACCTTC 325
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 244 GACTCTCTACCTCTCTCTCCGCGCTCCGCGGACGACGACGATTTGATTCATCCGACCTTC 303
 326 ATCGAGACGACGACGACGACGATTCGTCGGGATTCGATCCGCGGATTCGATCCGCGG 385
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 304 ATCGAGACGACGACGACGACGATTCGTCGGGATTCGATCCGCGGATTCGATCCGCGG 363
 386 TCCCTGGAGCCCAAGCCGAGAGAGATTCGATGATTCGATGATTCGATGATTCGATGATTC 445
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 364 TCCCTGGAGCCCAAGCCGAGAGAGATTCGATGATTCGATGATTCGATGATTCGATGATTC 423
 446 TATGCTTTACGCTTTGACGCGGATTCGATCCGCGGATTCGATCCGCGGATTCGATCCG 502
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 424 TATGCTTTACGCTTTGACGCGGATTCGATCCGCGGATTCGATCCGCGGATTCGATCCG 480

RESUT 9
 LOCUS BG238135
 DEFINITION sab2f07.y1 Gm-c1043 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1043-4093 5' similar to SW:GDI_ARATH P42751 CYCLIN DELTA-1.1, mRNA sequence.

ACCESSION BG238135
 VERSION BG238135.1 GI:12773208
 KEYWORDS EST.
 SOURCE soybean.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 533)
 Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kueba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Rheising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gidbons,M., Pape,D., Harvey,N., Schurk,R., Rilter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 Public Soybean EST Project
 Unpublished (1999)

TITLE Public Soybean EST Project
 JOURNAL Contact: Shoemaker R/Public Soybean EST Project
 COMMENT Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: estewatson.wustl.edu
 This clone is available through: Resgen, Invitrogen Corp. 2130 South Memorial Parkway Huntville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccul@resgen.com
 High quality sequence stop: 421.

FEATURES
 source
 1..533
 Location/Qualifiers
 /organism="Glycine max"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1043-4093"
 /clone_1lb="Gm-c1043"
 /tissue.type="Hypocotyl and Plumule, germinating seeds"
 /lab.host="DH10B"
 /note="Vector: pT73pac (Pharmacia); Site_1: EcoRI; Site_2: NotI; This cDNA library was constructed from mRNA isolated from hypocotyl and plumule tissues of seeds germinated for three days of the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a NotI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with EcoRI and NotI. The cDNA fragments were directionally cloned into the EcoRI-NotI restriction site of the pT73-Pac vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr.

Db	655	CTATGTTGTATGTA	670
RESULT 11			
LOCUS	BG886881	749 bp	mRNA linear EST 30-MAY-2001
DEFINITION	EST512732 cstd Solanum tuberosum tuberousm cdna clone cSTD214 5' sequence,		
ACCESSION	BG886881		
VERSION	BG886881.1	GI:14263967	
KEYWORDS	EST.		
SOURCE	Solanum tuberosum		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
REFERENCE	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
AUTHORS	Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
TITLE	1 (bases 1 to 749)		
JOURNAL	van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,Y., Chiemiango,A.;		
COMMENT	Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B. Generations of ESTs from dormant potato tubers Unpublished (2001) Contact: Cathy Ronning The Institute for Genomic Research For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdnaesgen.com Seq primer: M13F-R.		
FEATURES			
source	Location/Qualifiers 1..749 /organism="Solanum tuberosum" /cultivar="kennebec" /db_xref="taxon:4113" /clone="cSTD214" /clone_1ld="cSTD" /tissue_type="dormant tuber" /dev_stage="one month post-harvest" /lab_host="SOLR" /note="Vector: phuescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."		
BASE COUNT	197 a 181 c 146 g 225 t		
ORIGIN			
Query Match	16.9%; Score 382.8; DB 10; Length 749;		
Best Local Similarity	70.3%; Pred. NO. 4e-52;		
Matches 529;	Conservative 0; Mismatches 217; Indels 6; Gaps 1;		
OY	374 TTCAATCTCGTCCCTGGAGCGCAAGCCAGAGAATTCAGTTGATGATTCTCAAG	433	
bB	4 TTCACATCTCAATCTCTAAGGCCGCCGCTAGATGAATCGTGCAATGCATTCACAAG	63	
OY	434 GTACACGGCTACTATGAGCTTTGAGCTTTGAGGGGTACCTGCGGCTCACTATATGAT	493	
Db	64 GTACAAAGCACATATGTTTCCAGCATTAACGGCTATCTGCCGTTAACATTTTCAT	123	
OY	494 CGGTTTTGGATTCTGCGCGGTGGCGGAACAATAAGGTGGGCTCTGCACATTGTATCT	553	
OY	554 GTTGATGCTGTTCTTTGGCAGCAAAGATGGAAGAACCTCTGTGCATCTCTCTTGAC	613	
Db	124 CGTTCTCTACTACAGAAAGCTTGGCCGGAACAATAAGGTGGGCTCACTATATATTCG	183	
OY	614 CTTGAGATAGAAAGTGCCAATGATATTTTGAGCCGAGCAATTCGTGATGAGAGTA	673	
Db	244 CTTGAGGTTGAAGGGGCAAGATATATTATTTGAACAAAATGATTCACAAAGATGAGATT	303	
OY	674 CTGTGTTCTGCGTCTTAGATTGGAGGCTTAAGATCAATGACCACTTTCCTCGCT	733	

D6		TTTCTTGAGGATATTAGATTGGAGCGTCGCATCATCAACTCCGTTAGCTCCTACGT	363	
OY	734	TTCCTTGGCTGAAGAAGTAGATTCAAAGCTTTATCCGGTTCCTTAATCCAGGCCA	793	
D6	364	TTCCTTGGCGCTAAACCTTGATTCTACGTGGAACCTTTCATCCGTTCCTTAATCCAAGGGCT	423	
OY	794	ACACAATATCATGTAATGATAATATCCAGAGCGCTTTCCTTGCTACCTGACCCTTCAATGC	853	
D6	424	TCTCAGATTATTCCTCTCTAATATTCAGAACGACTGCTTTCATGATGATTTGGCCATCATGC	483	
OY	854	AATGCTGCTGCAGCACCATCACTCACTGACAGCTAATGAAAATTCCTAATGGTCTGTTTTAAG	913	
D6	484	AATAGCTGAGCTAACAAATCAATCATATGTCAGACTTAAGAGACCTTCCAAATTTCTCTTGAT	543	
OY	914	CCCCAAATTCGTGATGATCTGGTGGGAGGAGTAAGAAAAAGAAAAGTAATAGGTTGCTAC	973	
D6	544	GCTGAACATGCTGAATCTGCTGTATGATGACTCCACAAAGATATAAAATGCTGGCGCTAT	603	
OY	974	CAGTTGATGCAAGAGCTTGATTAACAAATPACCAACGGAAGTCCCCTTACTAAAGGT	1033	
D6	604	GAATTAGTGAGAGATGATGCAATTCATTAAGGCCCGCCAGAA-----TTTCCAAAGATA	657	
OY	1034	TTGCGGAGCGTCCGAGTAGTAACTACGAGCCGGAATGAGGTCAAGTACTGTTCATCATTC	1093	
D6	658	TACCCACAGGATGACAGTATGATGACGCGAGCTGATCTACTACTGATGAGCAATCAGTGAC	717	
OY	1094	TCATCATCTCTTCAACCTCCTCTCTCTTGC	1125	
D6	718	TCGTCGTCCTCATCATCATCTCTTCCACATC	749	
RESULT_12	B1432702	621 bp mRNA linear EST 21-Aug-2001		
LOCUS	B1432702	EST535463 P. infestans-challenged leaf Solanum tuberosum cDNA clone		
DEFINITION		PRAU06 5' sequence, mRNA sequence.		
ACCESSION	B1432702			
VERSION	B1432702.1	GI:15257392		
KEYWORDS	EST.			
SOURCE	Solanum tuberosum	potato.		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicts; Asterales; Eusterids I; Solanales; Solanaceae; Solanum. 1 (bases 1 to 621) Respiro,S., Griffiths,H.M., Smart,C.D., Cho,J., Chelmingo,A., Bouge,O., Buell,C.R., Roning,C.M., Fry,W.E. and Baker,B. Generation of ESTs from Potato Leaves Challenged with Phytophtora infestans, compatible interaction Unpublished (2000)	Contact: Cathy Kanning The Institute for Genomic Research For clone info: Please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@esgen.com Seq primer: M13F-R. Location/Qualifiers 1..621 organism="Solanum tuberosum" cultivar="Kenneduc" db_xref=taxon:"4113" clone="ppcaU06" clone_id="P. Infestans-challenged leaf" tissue_type="leaf" dev_stage="6 week old" lab_host="SOLR"		
JOURNAL COMMENT		/note=Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Whole plants were challenged with 450,000 sporangia/ml P. infestans US-1(US 940501) in Blottron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kenneduc plants showed no signs of HR. Katahdin plants (susceptible to P.		
FEATURES	source			

Db	476	TGAAGAGAAGAAACCAACAAGATATAATTAATAAAGCAACAGACGAGTAAAGCTGC	535
QY	1244	GCCAGATTGTCTAGAACCTCAA	1266
Db	536	CCCAAGCTGTCTAGAAACCTCAA	558
RESULT 14			
LOCUS	BGS26521	716 bp	mRNA linear EST 16-NOV-2001
DEFINITION	60-9 Stevia field grown leaf cDNA	Stevia rebaudiana	cDNA 5', mRNA sequence.
ACCESSION	BGS26521		
VERSION	BGS26521.1	GI:16950010	
KEYWORDS	EST,		
SOURCE	Stevia rebaudiana,		
ORGANISM	Stevia rebaudiana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae; Heliantheae; Stevia.		
AUTHORS	1 (bases 1 to 716)		
TITLE	Brandle,J.E., Richman,A., Swanson,A.K. and Chapman,B.P.		
JOURNAL	Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in diterpene synthesis		
COMMENT	Unpublished (2001) Contact: Jim Brandle Genomics and Biotechnology Agriculture and Agri-Food Canada - SCPPRC 1391 Sandford St., London, Ontario, CANADA, N5V 4T3 Tel.: 519 457 1470 Fax: 519 457 3997 Email: brandleje@em.agr.ca Seq primer: T3 promoter primer. Location/qualifiers 1..716 /organism="Stevia rebaudiana" /strain="751/1501" /cultivar="Iandrace" /db_xref="taxon:55670" /clone.lib="Stevia field grown leaf cDNA" /tissue.type="leaf" /dev_stage="field grown, mid-size" /lab_host="E. coli strain XLOR" /note="Vector: pBK-CMV; Site 1: EcoRI; site 2: XhoI; This cDNA library was constructed from poly(A) enriched mRNA from field grown leaves. Mid-size actively growing leaves were collected and pooled from several plants and frozen immediately after harvesting in liquid nitrogen. The cDNA was prepared using an XhoI-poly(dT) linker-primer. An EcoRI adapter was ligated to the blunt end cDNA and the products were digested with EcoRI and XhoI enabling directional cloning into the lambda ZAP Express vector. The library was amplified using the host strain XL1-Blue MRF. Mass excision of the library was performed to obtain pBK-CMV phagemid clones in the host strain XLOR. Single pass DNA sequencing was performed using the T3 promoter primer: 5' ATTAACCTTCATGAAGGGA 3'. This library was constructed by Alex Richman."		
BASE COUNT	186 a	154 c	157 g
ORIGIN			202 t
Query Match	13.2%;	Score 310.6;	DB 10; Length 716;
Best Local Similarity	69.2%;	Pred. No. 1,7e+40;	
Matches	454;	Conservative	0; Mismatches 199; Indels 3; Gaps 3
QY	331	GCAGAGCGCAACTTCGTTCC-GGGATTTCGACTACCTGTGGCGGTGCCAATTCGCTCCC	389
Db	9	GCACNAGMAAAGTGTCCTCCAAGAAATGATTAAGTCGAGGATTCATTCCAAGTTC	68
QY	390	TGGAGCCCAAGCCAGAGAAGATCAGTTGGATTCGATTCCTCAAGGTACACGGCTACTANG	449

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
Db	69	TCGAGGACATCTGCTAAGAAAGAAATCGTTGGCTCGGATGCTTAAAGGNCAGAGTTTTCACG	128									
Qy	450	GCATTACACCTTTGACGGCGTACTCGCCGCTCAACATATATGATGCGTTTTGGATTCTC	509									
Db	129	GATTTCACACCTTACGAGCGCTACCTCCGTCACACTACTCGATGCTTATCTATGTC	188									
Qy	510	GGCGGTTGGCCGGAACAAATGGGTGGGCTCTGCAACTGTATCTGTTGACATGCTGCTT	569									
Db	189	GGGCGCTTCCCGGTGGCAAAACGGGTGGCCCTTGCAACTCTTATCTGATTCAGCTTGNCCT	248									
Qy	570	TGGCAGCAAAAGATGAGAAAGAACCTCTTGTTCATCTCTCTTGGACCTTACATATAGAAAGTG	629									
Db	249	TAGCTGCTTAAATATGAGAGAAACATTTATTCCTTCATCTTGATCTTCAGGTGAAGGNG	308									
Qy	630	CCAAAGTACATATTTTGAAGCCGAGAACATATTCGTAGATGAGACTTACTTCTCGGTCT	689									
Db	309	CAAAATATATCTTTGAACCTTAAACAAATCCAAAGATATGAAATTTCTTACATGCTGCTT	368									
Qy	690	TAGATTTGAGGCTAAGATCATACATACACACTTGGTTCCTCGCTTCTTTCGCTCCAAAG	749									
Db	369	TGGATTTGAGGACTACGATCCGTTACACCGTTAGCTTATGGATATTTTTCGATTAAGA	428									
Qy	750	TAGATTTCAACAGGAACCTTTTATCCGGTCTCTTATTTCCAGGCAACAAATCATCATGAT	809									
Db	429	TGCGATCCATCTGGAATGTATATACGGGATTCCTTATCTCAAGGGCCAGCCAAATATTCAT	488									
Qy	810	CTAATATCCAAAGAGGCTAGCTTCTTCTGCTTACATGCGCCTTTCATGCAATTCGCTGACGCA	869									
Db	489	CAATATATCCAAAGAGCTAGTTACTTGAATATTTGGCCATCATCATGATTCAGCTGCAACCA	548									
Qy	870	TACTTACTGCGACGCTATATCAAAATTCCTAATTTGGTCTGTGCTTAAAGCCGAAATGCTGAGT	929									
Db	549	TACTTGGCGACGAGCAAGNATCTTCTTAAATTCCTCATCATCAATCCG-ACATGCGCAAT	606									
Qy	930	CATGGTGGGAGGACTAAGAAAAGAAAAGTAAATATGAGGCTGCTACACGATTGATGCNA	985									
Db	607	CATGGGNGATGGGCTCACAAAGAAAGATTCNAAATGTTCCAGATTANNGCNA	662									
RESULT	15											
LOCUS	BG597062											
DEFINITION	BG597062	728 bp	mRNA	linear	EST	12-APR-2001						
ACCESSION	BS1495740	cSTS	Solanum tuberosum	cdna	clone	cSTS161	5'	sequence,				
VERSION	BG597062											
KEYWORDS	BG597062.1	GI:13615202										
SOURCE	EST											
ORGANISM	potato.											
	Solanum tuberosum											
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;											
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;											
	Asteridae; easterides I; Solanales; Solanaceae; Solanum.											
	1 (bases 1 to 728)											
	van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,											
	Bouqir,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.											
	Generations of ESTs from sprouting potato eyes											
	unpublished (2000)											
	Contact: Cathy Ronning											
	The Institute for Genomic Research											
	for clone info: please contact Research Genetics, Libraries											
	Division tel 1-800-711-6195, email cdna@esgen.com											

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 25, 2002, 23:28:24 ; Search time 71 Seconds

(without alignments)
7815.297 Million cell updates/sec

Title: US-09-665-308D-11

Perfect score: 2259
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Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767056

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	53.4	2.4	7218	1	US-08-232-463-14
3	45.4	2.0	2417	1	US-08-011-398A-1
4	45.4	2.0	2417	1	US-08-464-051-1
5	45.4	2.0	2417	2	US-08-462-498-1
6	45.4	2.0	2417	3	US-08-554-385-2
7	44.2	2.0	2417	1	US-08-011-398B-1
8	44.2	2.0	2417	1	US-08-464-051-1
9	44.2	2.0	2417	2	US-08-462-498-1
10	44.2	2.0	2417	3	US-08-554-385-2
11	43.2	1.9	246240	2	US-08-724-394A-20
12	43.2	1.9	246240	2	US-08-724-394A-21
13	43.2	1.9	246240	2	US-08-724-394A-22
14	42.2	1.9	1215	2	US-09-092-770-8
15	42.2	1.9	1215	4	US-09-222-851-8
16	41	1.8	1798	2	US-08-557-128-12
17	39.8	1.8	549	1	US-07-991-867B-28
18	39.8	1.8	549	1	US-08-107-755A-28
19	39.8	1.8	549	2	US-08-544-332-8
20	39.8	1.8	1511	1	US-07-991-867B-8
21	39.8	1.8	1511	1	US-08-107-755A-8
22	39.8	1.8	1511	2	US-08-544-332-8
23	39.8	1.8	4810	3	US-08-852-629-11
24	39.8	1.8	4838	3	US-08-852-629-15
25	39	1.7	1212	2	US-09-092-770-18
26	39	1.7	1212	4	US-09-222-851-18
C 27	38.8	1.7	669	1	US-08-463-115-17

C 28	38.8	1.7	669	1	US-08-465-388-17	Sequence 17, Appl
C 29	38.6	1.7	388	2	US-08-623-906A-13	Sequence 13, Appl
C 30	38.4	1.7	296	1	US-08-738-367-8	Sequence 8, Appl1
C 31	38.2	1.7	1730	1	US-07-817-920-1	Sequence 1, Appl1
C 32	38.2	1.7	1730	1	US-08-117-006-1	Sequence 1, Appl1
C 33	38.2	1.7	1730	1	US-08-216-594-1	Sequence 1, Appl1
C 34	38.2	1.7	1730	5	PCT-US93-00149-1	Sequence 1, Appl1
C 35	38	1.7	1079	1	US-07-781-355-1	Sequence 1, Appl1
C 36	37.8	1.7	3380	2	US-09-156-425-1	Sequence 1, Appl1
C 37	37.6	1.7	593	4	US-09-385-982-262	Sequence 262, App
C 38	37.4	1.7	817	4	US-08-885-469-1	Sequence 1, Appl1
C 39	37.4	1.7	1554	2	US-08-031-538-8	Sequence 8, Appl1
C 40	37.4	1.7	1889	3	US-09-187-050-1	Sequence 1, Appl1
C 41	37	1.6	289	4	US-09-007-005-17	Sequence 17, Appl1
C 42	37	1.6	289	4	US-09-244-796-17	Sequence 17, Appl1
C 43	37	1.6	2862	4	US-08-569-749-13	Sequence 13, Appl1
C 44	37	1.6	2862	5	PCT-US96-12860-13	Sequence 13, Appl1
C 45	37	1.6	6124	4	US-08-213-419B-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHERFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BEWT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpc-fls
; US-08-232-463-14
Query Match 2.9%; Score 66; DB 1; Length 7218;

Best Local Similarity 3.8%; Pred. No. 7.9e-08;
Matches 15; Conservative 230; Mismatches 145; Indels 0; Gaps 0;

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OY 1133 AGGAGAAATTAATACCGTTTGGGTAGATGCAAGAACTCCGAGTAGAGAA 1192
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RESULT 2
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300, 6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
TELEPHONE: (703)836-9300
TELEFAX: (703)836-4109
TELEPHONE: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:

LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-Fls
US-08-232-463-14

Query Match 2.4%; Score 53.4; DB 1; Length 7218;
Best Local Similarity 2.4%; Pred. No. 0.0002;
Matches 9; Conservative 149; Mismatches 149; Indels 0; Gaps 0;

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OY 63 ACACCTCTCCGCGGACATCCGCTGAGGTCTCGGACCTCATGCGCAATGCGCATG 122
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Db 1125 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1184
OY 123 CCAACACATGAAATGCGAACCTCCGCTGCGCGGCTCTCATGTCGTTCCCTGCC 182
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OY 303 ATGTATATCGATCGAGCTTCATCGACGACGACGCAACTGCTCCGAGTTCGAGT 362
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OY 363 ACCTGTCGCGGTTCATCTC 383
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Db 1425 YYYYYYYYYYGTACCAATTC 1445
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RESULT 3
US-08-011-398B-1

Sequence 1, Application US/08011398B
Patent No. 5512473
GENERAL INFORMATION:
APPLICANT: Roger Brent
APPLICANT: Antonis S. Zervos
TITLE OF INVENTION: MAX-INTERACTING PROTEINS AND RELATED
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/011,398B
FILING DATE: 29 JAN 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162

RESULT 11
US-08-724-394A-20
; Sequence 20, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.

```

; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.COMTIG"
;
US-08-724-394A-20

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Best Local Similarity 45.2%; Pred. No. 0.71;
Matches 159; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

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QY 1334 TATGATATCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 1393
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DB 27213 TATTAACCTAATTTTACCTAAATAATTAATTAATTAATTAATTAATTAATTA 27272

QY 1394 TTTATGTTGGTACTTATTAATATGAGTTTCAGAAATTCACCTAGGAGGAGGATTTT 1453
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DB 27273 ATAGATTTTAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATA 27332

QY 1454 GCGACATGTTACCGTGGAGAGAAATGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 1513
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DB 27333 GCTATTAAGTAGAGACCAAAAGAAATATGAATATTTTACCCCAAAAAAAC 27392

QY 1514 GTTATGTTGGTACTTATTAATATGAGTTTCAGAAATTCACCTAGGAGGATTTT 1453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27393 TATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 27452

QY 1574 TGGGAGGATTTCAAGTTTGCAATTAATTAATTAATTAATTAATTAATTAATTA 1525
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27453 AAAACAGACCTTTGAGAGAGAGAAATTAATTAATTTGGGAGGATCCCAAGAA 27504

```

```

RESULT 12
US-08-724-394A-21
; Sequence 21. Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Krommal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.COMTIG"
;
US-08-724-394A-21

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Query Match      1.9%; Score 43.2; DB 2; Length 246240;
Best Local Similarity 45.2%; Pred. No. 0.71;
Matches 159; Conservative 0; Mismatches 193; Indels 0; Gaps 0;

QY 1274 TAGAGGTTTTGCAATTAATAATGACTGAGTGAGGTTGATTTATATATATATA 1333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27153 TAAATATTTGAATTTATTTAAATACCTAAATTCCTAAATATTTACATTAATTA 27212

QY 1334 TATGATATCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 1393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27213 TATTAACCTAATTTTACCTAAATAATTAATTAATTAATTAATTAATTAATTA 27272

QY 1394 TTTATGTTGGTACTTATTAATATGAGTTTCAGAAATTCACCTAGGAGGATTTT 1453
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27273 ATAGATTTTAAATTAATAATAATAATAATAATAATAATAATAATAATAATAATA 27332

QY 1454 GCGACATGTTACCGTGGAGAGAAATGAGAGAAAGAAAGAAAGAAAGAAAGAAAG 1513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 27333 GCTATTAAGTAGAGACCAAAAGAAATATGAATATTTTACCCCAAAAAAAC 27392

QY 1514 GTTATGTTGGTACTTATTAATATGAGTTTCAGAAATTCACCTAGGAGGATTTT 1573
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


Db 27393 TATTAATATACAGAGTATGATTCATGATGAGATCAAGATTGGAGATGACATTAAT 27452
Qy 1574 TGCAGGCTGGATTTCAGAGTTTGCATTAATTAATGCTGAAGAGATGAAAG 1625
Db 27453 AAAACAGAGACTTTGAGAGAGAAAATATATTTGGAGAGTCCCAAGAG 27504

RESULT 13

US-08-724-394A-22

; Sequence 22, Application US/08724394A
; Patent No. 5872237

; GENERAL INFORMATION:

; APPLICANT: Feder, John N.

; APPLICANT: Krommal, Gregory S.

; APPLICANT: Lauer, Peter M.

; APPLICANT: Ruddy, David A.

; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta

; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

; NUMBER OF INVENTIONS: Sequences and Antibodies Thereto

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,394A

; FILING DATE: 01-OCT-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Flits, Renee A.

; REGISTRATION NUMBER: 35,136

; REFERENCE/DOCKET NUMBER: 017957-000100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 246240 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: 1..246240

; OTHER INFORMATION: /note= "HLA-H.CONTIG"

; US-08-724-394A-22

Query Match 1.9%; Score 43.2; DB 2; Length 246240;
Best Local Similarity 45.2%; Pred. No. 0.71;
Matches 159; Conservative 0; Mismatches 193; Indels 0;

Qy 1274 TGAGGCTTTTGCATTAATAAAGCTTGAGTGGGCTGATTAATTAATAGTATATA 1333
Db 27153 TAAATTAATTTGATTTATTTAAATACCTAAATATCTAAATATTAATTAATTA 27212
Qy 1334 TATGATATATCTCTATACGATATATACAGAGATTGATGGTTGGAGTAAATTTTAT 1393
Db 27213 TATTACCTGAATTTTACCTAAATAAATAGATTTTAAATAAATTAATAAATAA 27272
Qy 1394 TTTATGTTGCTATATATATTTAGTTTGCAGATTCACCTAGGAGAGGATTTT 1453

Db 27273 ATAGATTTTAAATTAATAAATTAATGCAATAAGGCCCTAATATCTGCATCAT 27332
Qy 1454 GCGACATGTTTACCGTGGAGAGAAATGAGAGAAAGAAAGTGAACACTGACAGGG 1513
Db 27333 GCTTAAGTAGAGAGAGCAAGAAATTAATTAATTAATTTTACCACCTCAAAAAAC 27392
Qy 1514 GTAGAAATTTTAAATGATTTTGTCTTGTACCTGATTCGAGAAAGATTTGACT 1573
Db 27393 TATTAATATATACAGATATATGATTCATGCAATTCAGATTTGAGAGATGATTAAT 27452
Qy 1574 TGCAGGCTGGATTTCAGAGTTTGCATTAATTAATGCTGAAGAGATGAAAG 1625
Db 27453 AAAACAGAGACTTTGAGAGAGAAAATATATTTGGAGAGTCCCAAGAG 27504

RESULT 14

US-09-092-770-8

; Sequence 8, Application US/09092770
; Patent No. 5973119

; GENERAL INFORMATION:

; APPLICANT: Coats, Steven R.

; APPLICANT: Baas, Michael B.

; APPLICANT: Robinson, Murray O.

; TITLE OF INVENTION: No. 5973119el Cyclin E genes and proteins

; FILE REFERENCE: A-524

; CURRENT APPLICATION NUMBER: US/09/092,770

; CURRENT FILING DATE: 1997-06-05

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 8

; LENGTH: 1215

; TYPE: DNA

; ORGANISM: Human

; US-09-092-770-8

Query Match 1.9%; Score 42.2; DB 2; Length 1215;
Best Local Similarity 28.2%; Pred. No. 0.084;
Matches 131; Conservative 82; Mismatches 243; Indels 9; Gaps 2;

Qy 275 CCTCCTCCGCCGCTGCCGAGACAGAGATTTGATTCATCCGAGCTTCATCGACAC 334
Db 295 CCNNSNCCNYTNCNGAYTTNWSMTGGGNTGWSNARAGRTNGGYTNAAYATGYTN 354
Qy 335 GAGGCAACTCGTTCGGGATGTCAGTACCTGCGGGTTCATCGCTCCCTGGAC 394
Db 355 AARARAGARMSMGTATGTCATGATTAARCAATTTGARGTNTTNCAYMSNGAYTNGAR 414
Qy 395 GCCAAGCAGAGAGAGATGATGATGATTCATCAAGGTACAGCGGTACTATGCTTT 454
Db 415 CCNCARATGMSMGNATHYNTGATGATGATGATGATGATGATGATGATGATGATGAT 474
Qy 455 CAGCCTTTGAGCGGCTACCTGCGCGTCACTATATGATGATGATGATGATGATGATGAT 514
Db 475 CAYMNGARACNTTATYTTGNCARCAATYTTTAYGATGATGATGATGATGATGATGAT 529
Qy 515 TTGCGGGAACAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 574
Db 530 -AARARAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 588
Qy 575 GCAAGATGAGAACTCTTGTTCATCTCTCTTGGACCTTCAGATGAGATGAGTCCAG 634
Db 589 WSNARATGAGARATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
Qy 635 TACATATTTGAGCGGAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGAT 694
Db 646 GCGCCTGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 705
Qy 695 TGAGGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 739
Db 706 TGGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 750

RESULT 15

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US-09-222-851-8
: Sequence 8, Application US/09222851
: Patent No. 6165753
: GENERAL INFORMATION:
: APPLICANT: Coats, Steven R.
: APPLICANT: Bass, Michael B.
: APPLICANT: Robinson, Murray O.
: TITLE OF INVENTION: No. 6165753el Cyclin E Genes and Proteins
: FILE REFERENCE: A-524
: CURRENT APPLICATION NUMBER: US/09/222,851
: CURRENT FILING DATE: 1998-12-30
: EARLIER APPLICATION NUMBER: 09/092,770
: EARLIER FILING DATE: 1998-06-05
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 8
: LENGTH: 1215
: TYPE: DNA
: ORGANISM: Human
: US-09-222-851-8

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Query Match	1.9%	Score 42.2	DB 4	Length 1215
Best Local Similarity	28.2%	Pred. No. 0	DB4	
Matches 131	Conservative	82	Mismatches 243	Indels 9
				Gaps 2

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Db	295	CCMNSMCCNTYNTCCNGAYTWTMSTTGGGAGNTGYSMNARARGINTGGYTNAAATGYTN	354
OY	335	GAGCGCAACTTCGTCCGGGATTCGAGTACCTGTGCGCGGTTCCAAITCGCTCCCGGAC	394
Db	355	AARARARGARMNMONTAYGTNCAGAAARARAYTTGARGINTYNCAYMNSGAYTNGAR	414
OY	395	GCCAAAGCCAGAGAAGATCAGTTGGATGTTCTCGAAGTACGAGCTACTATGGCTT	454
Db	415	CCNCARATGMSNMNATHYTTTGATATGGTTNTTNCARGINTGYARGINTYACMYTN	474
OY	455	CAGCCTTGCAGGCGGTCACTCCGCGTCACTATATGAGATCGGTTTTGATTCGCGCG	514
Db	475	CAYMNGARCACTTATYATAYTNGCNCARGAYTTTTYTGAYMGNNTYATGYTNACMC	539
OY	515	TTGCCGGAACAATNGGTGGGCTCTCGCACTTATCTGTGTGATGCTCTGTCTTGCA	574
Db	530	-AARARGAYTHAAHYAAATAATGYTNCARTYNTTHGGNATHACMWSNNTYNTYATHGN	588
OY	575	GCAAAAGATGGAAGAACCTCTGTTCACATCTCTTGAGCTTCGATAGAGAGTGCCAG	634
Db	589	WSNAAHYTNGARGARATHTTATATGCMCCNAARTTNCARGARHTTYGC--NTATGYTACAGAT	645
OY	635	TACATATTTTGAGCCGAGAACCAATTCGTAGCATGAGCTACTTGTTCGGGTGCTTAGAT	694
Db	646	GGNGCNTGYWNSNGARGAGATATHTYTMGNATGAGARFTNATHATHTYNAARGCNYTNAAR	705
OY	695	TGGAGGCTTAAGATCAGTATACACCACTTTGCTTCCTCGCTTCTCTT	739
Db	706	TGGGARNTNTGYCCGATACNATATHTATMNSNTGTYTNAAYTNTTY	750

Search completed: October 26, 2002, 01:39:56
Job time : 294 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 14:34:14 ; Search time 34 Seconds
(without alignments)
1107.471 Million cell updates/sec

Title: us-09-665-308d-12

Perfect score: 1758
Sequence: 1 MSVSCSLSDVLLCGEDSGT.....SCKRRKLNNRLNWDKGNSE 339

Scoring table: BLASTSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_032802.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1758	100.0	339	AA19894	soybean cyclin del
2	1262	71.8	318	AA19895	soybean cyclin del
3	1030	58.6	328	AA19896	Arabidopsis thalia
4	1030	58.6	339	AA19897	Arabidopsis thalia
5	1011	57.5	320	AA19898	Arabidopsis thalia
6	502.5	28.6	358	AA19899	Maize cyclin D. Z
7	496.5	28.2	358	AA19900	Maize cyclin D. Z
8	470	26.7	390	AA19901	Maize cyclin D. Z
9	467	26.6	388	AA19902	Corn cyclin delta-
10	420.5	23.9	308	AA19903	Arabidopsis thalia
11	419.5	23.9	307	AA19904	Arabidopsis thalia

12	419.5	23.9	367	AA19905	Arabidopsis thalia
13	418.5	23.8	308	AA19906	Arabidopsis thalia
14	411	23.4	361	AA19907	Arabidopsis thalia
15	411	23.4	361	AA19908	Arabidopsis thalia
16	410.5	23.4	308	AA19909	Arabidopsis thalia
17	406	23.1	287	AA19910	Arabidopsis thalia
18	404	23.0	287	AA19911	Arabidopsis thalia
19	402.5	22.9	273	AA19912	Arabidopsis thalia
20	400.5	22.8	273	AA19913	Arabidopsis thalia
21	396.5	22.6	308	AA19914	Arabidopsis thalia
22	396.5	22.6	308	AA19915	Arabidopsis thalia
23	340	19.3	349	AA19916	Maize cyclin D. Z
24	318.5	18.1	238	AA19917	Maize cyclin D. Z
25	305.5	17.4	262	AA19918	Arabidopsis thalia
26	305.5	17.3	240	AA19919	Arabidopsis thalia
27	305	17.3	240	AA19920	Arabidopsis thalia
28	295	16.8	263	AA19921	Arabidopsis thalia
29	272.5	15.5	232	AA19922	Arabidopsis thalia
30	272.5	15.5	232	AA19923	Arabidopsis thalia
31	267.5	15.2	181	AA19924	Rice cyclin delta-
32	255	14.5	318	AA19925	Corn cyclin delta-
33	251	14.3	341	AA19926	Arabidopsis thalia
34	250.5	14.2	307	AA19927	Arabidopsis thalia
35	247.5	14.1	298	AA19928	Arabidopsis thalia
36	221	12.6	509	AA19929	Arabidopsis thalia
37	199.5	11.3	424	AA19930	Protein Involved I
38	197	11.2	420	AA19931	Human cancer assoc
39	196	11.1	398	AA19932	A cyclin related p
40	196	11.1	398	AA19933	Human protein sequ
41	194.5	11.1	146	AA19934	Arabidopsis thalia
42	194.5	11.1	146	AA19935	Arabidopsis thalia
43	194.5	11.1	257	AA19936	Arabidopsis thalia
44	194	11.0	481	AA19937	Drosophila melanog
45	184.5	10.5	421	AA19938	Novel human diagno

ALIGNMENTS

RESULT 1
AA19894
ID AA19894 standard; Protein; 339 AA.
XX
AC AA19894;
XX
DT 21-DEC-1999 (first entry)
XX
DE soybean cyclin delta-1.
XX
KW Cyclin delta-1; soybean; cell cycle; cell division;
KW transgenic plant; herbicide; plant breeding.
XX
OS Glycine max.
XX
PN W0994486-A2.
XX
PD 30-SEP-1999.
XX
PF 19-MAR-1999; 99MO-US06047.
XX
PR 23-MAR-1998; 98US-0078948.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Klein TM, Odell JT, Orozco EW;
XX
DR WPI: 1999-591036/50.
XX
DR N-PSDB; AA19938.
XX
PT New isolated plant cyclin genes, used to develop products for use as
XX herbicides and for developing plant breeding programs -
XX
PS Claim 6; Page 52-53; 68pp; English.

XX This is the deduced amino acid sequence of a corn cyclin delta-1
CC protein derived from the nucleotide sequence (see AA219958) of a
CC contig composed of clones isolated from soybean libraries. It
CC herbicide-sprayed and soybean root ear CDNA libraries. It
CC represents the entire protein. The invention relates to isolated
CC nucleic acid fragments (see AA219953-66) encoding cyclin A, cyclin
CC delta-1, cyclin delta-2 and cyclin delta-3 polypeptides (see
CC AA21889-902). It also relates to the construction of chimeric genes
CC encoding all or a portion of a cyclin, in sense or antisense
CC orientation, where expression of the chimeric gene results in altered
CC levels of the cyclin protein in a transformed host cell. This would
CC have the effect of altering the regulation of cell division in those
CC cells. The nucleic acid fragments may be used to express cyclins in
CC plant cells to enhance cell tissue culture growth. The availability
CC of nucleic acid sequences encoding all or a portion of cyclins should
CC facilitate studies of cell cycle in plants, provide genetic tools
CC to enhance cell growth in tissue culture, increase the efficiency
CC of gene transfer and help provide more stable transformations. The
CC proteins can be used as targets to facilitate design and/or
CC identification of inhibitors of those enzymes that may be useful as
CC herbicides.

XX Sequence 339 AA;

Query Match 100.0%; Score 1758; DB 20; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.6e-185;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVSLSTYDLICGDDSGIISGESPECSFSIDSSPPPTTDDCYSIASFIERHNF 60
DB 1 MSVSLSTYDLICGDDSGIISGESPECSFSIDSSPPPTTDDCYSIASFIERHNF 60
QY 61 VPGEFYLSRFSRSDANARESVGMILKVHAYYGFOPITAYLVNMDRFLDSRLPPT 120
DB 61 VPGEFYLSRFSRSDANARESVGMILKVHAYYGFOPITAYLVNMDRFLDSRLPPT 120
QY 121 NGMPLOLVSVACISLAAMEEPLVPSLIDLOIEGAKYIFEPRTIRRMELLVGLVDMRLR 180
DB 121 NGMPLOLVSVACISLAAMEEPLVPSLIDLOIEGAKYIFEPRTIRRMELLVGLVDMRLR 180
QY 181 SVTPICLTAFACKVDSTGTFTIRFLISRATETIIVSNIOGASFLAYWPCISIAAAIITAN 240
DB 181 SVTPICLTAFACKVDSTGTFTIRFLISRATETIIVSNIOGASFLAYWPCISIAAAIITAN 240
QY 241 EIPNMSVYKPENAESWCEGLRKEKYGICYQLMOELVINNORLPLKVLPLQRLVTTTR 300
DB 241 EIPNMSVYKPENAESWCEGLRKEKYGICYQLMOELVINNORLPLKVLPLQRLVTTTR 300
QY 301 MRSSVYSSFSSTSTFSLSCRRKRLNNRLVWDDKGNSE 339
DB 301 MRSSVYSSFSSTSTFSLSCRRKRLNNRLVWDDKGNSE 339

RESULT 2

AA21895
ID AA21895 standard; Protein; 318 AA.

XX AA21895;

DT 21-DEC-1999 (first entry)

XX Soybean cyclin delta-1 partial polypeptide.

XX Cyclin delta-1; soybean; cell cycle; cell division;

KW transgenic plant; herbicide; plant breeding.

OS Glycine max.

PN MO9948486-A2.

PD 30-SEP-1999.

PF 19-MAR-1999; 99WO-US06047.
XX
PR 23-MAR-1998; 98US-0078948.
XX
PA (DUPD) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Klein TM, Odell JT, Orozco EM;
XX
DR WPI: 1999-591036/50.
DR N-PSDB; AA219959.

PT New isolated plant cyclin genes, used to develop products for use as
herbicides and for developing plant breeding programs -
XX
XX Claim 6; Page 54-55; 68pp; English.

XX This is the deduced amino acid sequence of a corn cyclin delta-1
CC protein derived from the nucleotide sequence (see AA219959) of a
CC clone isolated from a soybean embryo CDNA library. It represents
CC 95% of the entire protein. The invention relates to isolated
CC nucleic acid fragments (see AA219953-66) encoding cyclin A, cyclin
CC delta-1, cyclin delta-2 and cyclin delta-3 polypeptides (see
CC AA21889-902). It also relates to the construction of chimeric genes
CC encoding all or a portion of a cyclin, in sense or antisense
CC orientation, where expression of the chimeric gene results in altered
CC levels of the cyclin protein in a transformed host cell. This would
CC have the effect of altering the regulation of cell division in those
CC cells. The nucleic acid fragments may be used to express cyclins in
CC plant cells to enhance cell tissue culture growth. The availability
CC of nucleic acid sequences encoding all or a portion of cyclins should
CC facilitate studies of cell cycle in plants, provide genetic tools
CC to enhance cell growth in tissue culture, increase the efficiency
CC of gene transfer and help provide more stable transformations. The
CC proteins can be used as targets to facilitate design and/or
CC identification of inhibitors of those enzymes that may be useful as
CC herbicides.

XX Sequence 318 AA;

Query Match 71.8%; Score 1362; DB 20; Length 318;
Best Local Similarity 78.2%; Pred. No. 3.2e-130;
Matches 255; Conservative 29; Mismatches 28; Indels 14; Gaps 7;

QY 18 SGILSESPSCFSIDSSPPPTTDDCYSIASFIERHNVPEFYLSRFSRSDA 77
DB 3 AGIMD-SSPECS-SDIDSSPP-----SEAESIAGMEDEERNVPEFYLSRFSRSDA 54
QY 78 NAREESVGMILKVHAYYGFOPITAYLVNMDRFLDSRLPPTNGMPLQVSVACTSLA 136
DB 55 SAREESVGMILKVHAYYGFOPITAYLVNMDRFLDSRLPPTNGMPLQVSVACTSLA 114
QY 137 AKKEEPLVPSLIDLOIEGAKYIFEPRTIRRMELLVGLVDMRLSVTPICLTAFACKVD 196
DB 115 AKKEEPLVPSLIDLOIEGAKYIFEPRTIRRMELLVGLVDMRLSVTPICLTAFACKVD 174
QY 197 STGTFTIRFLISRATETIIVSNIOGASFLAYWPCISIAAAIITAN 256
DB 175 STGTFTIRFLISRATETIIVSNIOGASFLAYWPCISIAAAIITAN 234
QY 257 CEGLRKEKYGICYQLMOELVINNORLPLKVLPLQRLVTTTRMRSSVYSS--SSSS 314
DB 235 CEGLRKEKYGICYQLMOELVINNORLPLKVLPLQRLVTTTRMRSSVYSS--SSSS 292
QY 315 TSFSLSCRRKRLNNRLVWDDKGNSE 339
DB 293 SSSSLSCRRKRLNNRLVWDDKGNSE 318

RESULT 3

AA29789
ID AA29789 standard; Protein; 328 AA.

XX AA29789;

XX 17-OCT-2000 (first entry)
DN
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35502.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 07-MAY-1999; 99US-0132487.
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PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
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PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 18-JUN-1999; 99US-0139456.
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PR 18-JUN-1999; 99US-0139459.
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PR 18-JUN-1999; 99US-0139461.
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PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
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PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
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PR 28-JUN-1999; 99US-0140695.
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PR 01-JUL-1999; 99US-0141287.
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PR 01-JUL-1999; 99US-0142154.
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PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
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PR 14-JUL-1999; 99US-0143624.
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PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
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PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 28-JUL-1999; 99US-0145919.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147132.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149358.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.

[illegible]

RESULT 4	
AA629788	
ID	AA629788 standard; Protein: 339 AA.
XX	
AC	AA629788;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 35501.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence.
KW	
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.
PR	23-APR-1999; 99US-0130510.
PR	23-APR-1999; 99US-0130891.
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PR	20-MAY-1999; 99US-0135124.
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PR	01-JUN-1999; 99US-0137222.
PR	03-JUN-1999; 99US-0137528.
PR	04-JUN-1999; 99US-0137502.
PR	07-JUN-1999; 99US-0137724.
PR	08-JUN-1999; 99US-0138094.
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PR	10-JUN-1999; 99US-0138847.
PR	14-JUN-1999; 99US-0139119.

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PR 12-AUG-1999; 99US-0148341.
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 PR 22-OCT-1999; 99US-0160981.
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 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161993.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 58.6%; Score 1030; DB 21; Length 339;
 Best Local Similarity 63.3%; Pred. No. 1,3e-104;
 Matches 214; Conservative 44; Mismatches 62; Indels 18; Gaps 7;
 QY 1 MSVSCSLSDYDLGCGDSSGILGSESP-ECFSFSDIDSSPPPPPTTDCYISINSFIEHKN 59
 DB 12 MSVSFSDMDLPCGED-SCVFSGSESTVDFSSSEVDSWPCD-----SIACFIEDRH 61

CC CycD binds to CDK4, and the active CycD-CDK4 hyperphosphorylates
 CC retinoblastoma associated protein, releasing the E2F transcription
 CC factor which activates DNA synthesis. The invention provides maize
 CC CycD polynucleotides (see AA294581-84) and polypeptides (see
 CC AA29321-24) that are involved in cell cycle regulation. Also provided
 CC are recombinant expression cassettes (including ZmCycD in sense or
 CC antisense orientation), host cells, transgenic plants (especially
 CC corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or
 CC oilseed Brassica) and antibody compositions. A claimed method of
 CC modulating the level of CycD protein in a cell comprises
 CC transforming the cell with a recombinant expression cassette
 CC comprising a CycD polynucleotide linked to a promoter, and
 CC growing the cell for a time sufficient to induce expression of the
 CC polynucleotide sufficient to modulate (increase or decrease) the
 CC CycD protein in the cell. The CycD protein is present in an amount
 CC sufficient to alter cell division, increase the number of cells
 CC dividing, improve transformation frequencies, alter cell growth,
 CC increase the growth rate, increase crop yield, alter plant
 CC height or size, enhance or inhibit organ (seed, root, shoot, ear,
 CC tassel, stalk, pollen, stamen) growth, produce organ ablation,
 CC produce parthenocarpic fruits, produce male sterile plants,
 CC enhance embryogenic response, increase callus induction, provide
 CC positive selection, increase plant regeneration, alter the time
 CC that cells are arrested in G1 or G0 phase or in a particular cell
 CC cycle, improve response to environmental stress including
 CC dehydration, heat or cold, increase the number of pods per plant,
 CC increase the number of seeds per pod or ear, alter the lag time in
 CC seed development, provide hormone-independent cell growth, or
 CC increase the growth rate of cells in bioreactors. The level of
 CC CycD protein in the cells is transiently modulated by introducing
 CC CycD RNA or CycD polypeptides. All claimed.

XX Sequence 358 AA;

Query Match 28.6%; Score 502.5; DB 21; Length 358;
 Best Local Similarity 34.0%; Pred. No. 1.9e-46;
 Matches 131; Conservative 60; Mismatches 99; Indels 95; Gaps 11;

QY 9 YD-----LLCGEDSSGI--LSGESPECSFSDIDSSPPSP----- 43
 DB 5 YCAASVLLCARNMAIIGLDDGESSWA---AATPRDVIYAAAMATGVAVDGILTEF 61
 QY 44 ---TEDCVSIASFIEHENVTFGEFYLSFQSGRSD---ANARESGVMILKVHAYYGFQ 97
 DB 62 PLISDCC--VATLVEKEVHMPAEGLQKLRHGDLLAAVRKDAIMWIMVIEHYNDA 119
 QY 98 PLTAVALVAVMDRFLDSRLPTNGMPLOLVACTSLAAKMEEDLVSLDIOTEGAKY 157
 DB 120 PLTAVALSVYLDRELFSTEFPEGRAMTQLLAVACLSTASKTEEFVPLDLOVAEAKF 179
 QY 158 IFEPTIRRMEDLVGLVDMRLSVTPLCFLAFACKYDSTGTETRFISRATEIIVANI 217
 DB 180 VPEGRIKMEELVLTSLKWRHNAVTAQSFVEYFLHKLSDHGAPSLARSNSDLVSTA 239
 QY 218 QDASFLAYPSCIAAAIITLANETPNMSVAKPENAESWCESGLREKXYGYCYOLMOELVT 277
 DB 240 KCAEEVVPSPETIAAIVLAIGECRS--SVI--EBAASSCYLDERVLRCHEMIOE--- 293
 QY 278 NNNOKRLPLKYLPLQRLVTRTRMRSSVYSSRSS----- 311
 DB 294 -----KITAGSIVLKSAGSSISVPSQPIGVLDAAACLQQSDDATVGS 337
 QY 312 -----SSSTFSLSCKRKLNNRL 330
 DB 338 PAVCYHSSST-----KRRRITRRL 357

RESULT 7
 AAY79322
 ID AAY79322 standard; Protein; 358 AA.
 XX
 AC AAY79322;
 XX

DT 18-JUL-2000 (first entry)
 XX
 DE Maize cyclin D.
 XX
 KW Maize; cyclin D; ZmCycD; CycD; cell division; cell cycle;
 XX transgenic plant.
 XX
 OS Zea mays.
 XX
 PN W0200017364-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 21-SEP-1999; 99WO-US21946.
 XX
 PR 23-SEP-1998; 98US-0101551.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McEliver JA;
 PI Hoerster GJ;
 XX
 DR WPI; 2000-283589/24.
 DR N-PSDB; AA294582.
 XX
 PT Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,
 PT related proteins and antisense RNA useful for control of cell cycle
 PT regulation
 XX
 PS Claim 16; Page 121-122; 134pp; English.

CC The present sequence is that of an isoform of maize cyclin D
 CC (CycD), a protein necessary for progression from G1 into S phase.
 CC CycD binds to CDK4, and the active CycD-CDK4 hyperphosphorylates
 CC retinoblastoma associated protein, releasing the E2F transcription
 CC factor which activates DNA synthesis. The invention provides maize
 CC CycD polynucleotides (see AA294581-84) and polypeptides (see
 CC AA29321-24) that are involved in cell cycle regulation. Also provided
 CC are recombinant expression cassettes (including ZmCycD in sense or
 CC antisense orientation), host cells, transgenic plants (especially
 CC corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or
 CC oilseed Brassica) and antibody compositions. A claimed method of
 CC modulating the level of CycD protein in a cell comprises
 CC transforming the cell with a recombinant expression cassette
 CC comprising a CycD polynucleotide linked to a promoter, and
 CC growing the cell for a time sufficient to induce expression of the
 CC polynucleotide sufficient to modulate (increase or decrease) the
 CC CycD protein in the cell. The CycD protein is present in an amount
 CC sufficient to alter cell division, increase the number of cells
 CC dividing, improve transformation frequencies, alter cell growth,
 CC increase the growth rate, increase crop yield, alter plant
 CC height or size, enhance or inhibit organ (seed, root, shoot, ear,
 CC tassel, stalk, pollen, stamen) growth, produce organ ablation,
 CC produce parthenocarpic fruits, produce male sterile plants,
 CC enhance embryogenic response, increase callus induction, provide
 CC positive selection, increase plant regeneration, alter the time
 CC that cells are arrested in G1 or G0 phase or in a particular cell
 CC cycle, improve response to environmental stress including
 CC dehydration, heat or cold, increase the number of pods per plant,
 CC increase the number of seeds per pod or ear, alter the lag time in
 CC seed development, provide hormone-independent cell growth, or
 CC increase the growth rate of cells in bioreactors. The level of
 CC CycD protein in the cells is transiently modulated by introducing
 CC CycD RNA or CycD polypeptides. All claimed.

XX Sequence 358 AA;

Query Match 28.2%; Score 496.5; DB 21; Length 358;
 Best Local Similarity 33.8%; Pred. No. 8.8e-46;
 Matches 130; Conservative 60; Mismatches 100; Indels 95; Gaps 11;
 QY 9 YD-----LLCGEDSSGI--LSGESPECSFSDIDSSPPSP----- 43
 DB 5 YCAASVLLCARNMAIIGLDDGESSWA---AATPRDVIYAAAMATGVAVDGILTEF 61

Db 5 YDCAASVTLCAEDNAAILGLDDDEESSMA---AAATPPRDVAAAATGYAVDGLTLEF 61

Qy 44 ---TEDCYSIASFIEHENFVPGGEYLSRPSRLDAN---AREESGMILKHAAYGFO 97

Db 62 PLUSDCC-VATLVEKEVHEHNPARGYLQKLDORRHDDLDLAVVRDADIMKRYIEHNF 119

Qy 98 PLTAVLAVNWDRLFDLSRRLPETNGWPLQVSVACLSTAAKMEBPLVPSLDLQIEGAKY 157

Db 120 PLTAVLSVNYDLRFLSTYEPEPGRAMMHTQLLAVACLSTASKIEETFEVLEFLDLQVAEAKF 179

Qy 158 IFEERTIRRMILLVGLVDMLRBSVTPLCFLAFRCAKDSGTGTFIRLISATELIVSNI 217

Db 180 VFEERTIRRMILLVSLTKRMAHVAVTACSFPEYFLHKISDHGAPSLARSSSDVLVSTA 239

Qy 218 QEASFLAYWPSGCIAAAAILTAAINEIPNMSVYKPERNAESMCEGLREKVIQCYQLMQELVI 277

Db 240 KGAEFVYFRPEELASVALAIGCGRS-SYI--EBAASSCKYLDKERLKHENKQE--- 293

Qy 278 NNNOKRLPLKLVLPQLRVTTRFRNRSGTVSSFS----- 311

Db 294 -----SSSTSFSLCKRRKRNLR 330

Qy 312 -----KITGSIYLYKSAGSSISVPOSPIGVLDAACLSODSDATVGS 337

Db 338 PAVCYHSSSTS-----KRRMITRRL 357

RESULT 8

AA79323

ID AA79323 standard; Protein: 390 AA.

XX AA79323:

XX 18-JUL-2000 (first entry)

XX Maize cyclin D.

XX Maize: cyclin D; ZmCycD; CycD; cell division; cell cycle;

XX Transgenic plant.

XX Zea mays.

XX WO200017364-A2.

XX 30-MAR-2000.

XX 21-SEP-1999; 99WO-US21946.

XX 23-SEP-1998; 98US-0101551.

XX (PION-) PIONEER HI-BRED INT INC.

XX Lowe KS, Tao Y, Gordon-Kamm WJ, Gregory CA, McElver JA;

XX Hoerster GJ;

XX WPI: 2000-283589/24.

XX N-PSDB: AA294583.

XX Novel polynucleotides encoding maize cyclin D isoforms 1, 2 and 3,

XX related proteins and antisense RNA useful for control of cell cycle

XX regulation -

XX Claim 16; Page 124-125; 134pp; English.

CC The present sequence is that of an isoform of maize cyclin D

CC (CycD), a protein necessary for progression from G1 into S phase.

CC CycD binds to CDK4, and the active CycD-CDK4 hyperphosphorylates

CC retinoblastoma associated protein, releasing the E2F transcription

CC factor which activates DNA synthesis. The invention provides maize

CC CycD polynucleotides (see AA294581-84) and polypeptides (see

CC AA79321-24) that are involved in cell cycle regulation. Also provided

CC are recombinant expression cassettes (including ZmCycD in sense or

CC antisense orientation), host cells, transgenic plants (especially

	CC	corn, sorghum, sunflower, safflower, wheat, rice, alfalfa or
	CC	crossed brassica) and antibody compositions. A claimed method of
	CC	modulating the level of CycD protein in a cell comprises.
	CC	transforming the cell with a recombinant expression cassette
	CC	comprising a CycD polynucleotide linked to a promoter, and
	CC	growing the cell for a time sufficient to induce overexpression of the
	CC	polynucleotide sufficient to modulate (increase or decrease) the
	CC	CycD protein in the cell. The CycD protein is present in an amount
	CC	sufficient to alter cell division. increase the number of cells
	CC	dividing, improve transformation frequencies, alter plant growth,
	CC	increase the growth rate, increase crop yield, alter plant
	CC	height or size, enhance or inhibit organ (seed, root, shoot, ear,
	CC	tassel, stalk, pollen, stamen) growth, produce organ ablation,
	CC	produce parthenocarpic fruits, produce male sterile plants,
	CC	enhance embryogenic response, increase callus induction, provide
	CC	positive selection, increase plant regeneration, alter the time
	CC	that cells are arrested in G1 or G0 phase or in a particular cell
	CC	cycle, improve response to environmental stress including
	CC	dehydration, heat or cold, increase the number of pods per plant,
	CC	increase the number of seeds per pod or ear, alter the lag time in
	CC	seed development, provide hormone-independent cell growth, or
	CC	increase the growth rate of cells in bioreactors. The level of
	CC	CycD protein in the cells is transiently modulated by introducing
	CC	CycD RNA or CycD polypeptides. All claimed.
XX	Sequence	390 AA:
SQ		
	Query Match	26.7%: Score 470; Db 21; Length 390;
	Best Local Similarity	33.6%: Pred. No. 8,3e-43;
	Matches 130;	Conservative 59; Mismatches 124; Indels 74; Gaps 13.
OY		1 MSVSCISLDVD-----LLCEDSSGIL-----SGSPDCSFSF---IDSSP 37
Db		1 MAPSC--YDAASMLCAEEHSSILTWDEEERLEAVGRRRGRSP--GYGDGFADLFP 55
OY		38 PPSPTPEDCYSTASTIEHRNPNVGFEFLSPQRSRLDANARESYGIITXVAYAYGQ 97
Db		56 -----POSEEC--VAGIVERDRHMFOPCYCDLRKGGGCCLCVREAVDWIKATTHRRR 109
OY		98 PLTAYTLAVNTMRFLDSRRILPETNGMPLQOLVSACLSLAARKEELPVSLDLQIBGAKY 157
Db		110 PLTAYTLAVNTYDLFSLSEVPDGKDMMQTLAVACVSLAAKEETAAPQCILDVGDARY 169
OY		158 IFERTIRRMELLVLGVLDWRLRSYTPICFLAFACKYDSGTFT--RFLSRATEIIVS 215
Db		170 VFEKTYQRRELLLYLTLLNMRAHYLPESYDVYFNKRLSNGSTRAPNSCWLDQSAEDLR 229
OY		216 NIOGASFIAWPSCIAAAAAILTAANEIPMWSVVKENAESMCDELIREKYIGCYQLMOEL 275
Db		230 AARGTCGVGRPBEIAAAAAVAAGVDADADV--EMN--CCAIVDERVILROGEALGSM 285
OY		276 V-----INNORKLPLKYLPOLRV-----TTRTMR 302
Db		286 ASSAAMDIGDATVPKRGARRRSSPPVPVPVPGVGLDAACLSYSEEAATATTSAA 345
OY		303 SSTYSPFSSTSSSTSLSCKRKRLNR 329
Db		346 SHGPPGSSSSSTS-FYTSKRKKLASR 371
RESULT 9		
AAAY31897		
ID		AAVJ31897 standard; Protein; 388 AA.
XX		AAVJ31897:
XX		21-DEC-1999 (first entry)
XX		Corn cyclin delta-2 partial polypeptide.
XX		Cyclin delta-2; corn; maize; cell cycle; cell division;
XX		transgenic plant; herbicide; plant breeding.

OS Zea mays.
XX WO9948486-A2.
PN
XX
PD 30-SEP-1999.
XX
PF 19-MAR-1999; 99MO-US06047.
XX
PR 23-MAR-1998; 98US-0078948.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Klein TM, Odell JT, Orozco EM;
XX
DR WPI; 1999-591036/50.
XX N-PSDB; AAZ19961.
PT
PT New isolated plant cyclin genes, used to develop products for use as
PS herbicides and for developing plant breeding programs -
PS
PS Claim 11, Page 56-57; 68pp; English.
XX
XX This is the deduced amino acid sequence of a corn cyclin delta-2
CC protein derived from the nucleotide sequence (see AA219961) of a
CC clone from an embryo leaf cDNA library. It represents 94% of the
CC full-length protein. The invention relates to isolated nucleic
CC acid fragments (see AA219953-66) encoding cyclin A, cyclin delta-1,
CC cyclin delta-2 and cyclin delta-3 polypeptides (see AA21889-902).
CC It also relates to the construction of chimeric genes encoding all
CC or a portion of a cyclin, in sense or antisense orientation, where
CC expression of the chimeric gene results in altered levels of the
CC cyclin protein in a transformed host cell. This would have the
CC effect of altering the regulation of cell division in those cells.
CC The nucleic acid fragments may be used to express cyclins in plant
CC cells to enhance cell tissue culture growth. The availability of
CC nucleic acid sequences encoding all or a portion of cyclins should
CC facilitate studies of cell cycle in plants, provide genetic tools
CC to enhance cell growth in tissue culture, increase the efficiency
CC of gene transfer and help provide more stable transformations. The
CC proteins can be used as targets to facilitate design and/or
CC identification of inhibitors of those enzymes that may be useful as
CC herbicides.
CC
XX
XX Sequence 388 AA:
SQ
Query Match 26.6%; Score 467; DB 20; Length 388;
Best Local Similarity 34.1%; Pred. No. 1,8e-42;
Matches 131; Conservative 62; Mismatches 121; Indels 70; Gaps 14;
QY 1 MSVSGLSDYD-----LIGGEDSSGIL-----SGESPECSFSD---IDSSP 37
DB 1 MAPSC---YDAAASMLCAEHSSTILWYEEEEELEAVGRNSGRSP--GYGDPCADLFP 55
QY 38 PPPSTTECKYSIASFIEHNFVPGFEXLSRFQSRSLDANAREBSVGLTVHAYYGFQ 97
DB 56 ----FQSEEC--VAGLVEHERHMPGCGDRLRGSGGCLCYRREAVDVIWATYTHRRR 109
QY 98 PLTAVLAVNYMDRLFDRLRPETNGPVLQVSVACISLAAKKEBPLVPSLDLQIG-AK 156
DB 110 PLTAVLAVNYLDRFLSLSEVPDCKDMTQLLAVACVSLAAKKEETAVPCDLQOEGDAR 169
QY 157 YFEPRTIRMLLVGLVDMLRSTYPLCFAPACKYDSTGTF--NFLSRATEIIV 214
DB 170 YVEFAKTYQRMELVLTJTNMRHAAVTSPSYDYFLNKLNNGSTAPRSCWMLQSAELII 229
QY 215 SNIQESFLAYWPCITAAAAIITLANEIPNMWSYKPEENSMCEGLRKEKEVCYQIMOE 274
DB 230 RAARGTGVGFPSSETAAVAANAACVDADGV--ENA--CCAHYDKERYLFCQDAIGS 285
QY 275 LV-----INNQRKLPLKLVLPOL-----RVTRTRMRSSTVS- 307
DB 286 MASSAAIDATVPPKSARRRSSVPVQSPVGLDAAPCLSTYSEEAATATATATSAASH 345

QY 308 --SFSSSSSTFSLSCKRRRLNMR 329
DB 346 GAGSSSSSSSTFPTSKRRKLASR 369
RESULT 10
AAG47103
ID AAG47103 standard; Protein: 308 AA.
XX
XX AAG47103;
AC
XX 18-OCT-2000 (first entry)
DT
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59333.
XX
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
XX EP1033405-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
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PR 14-MAY-1999; 99US-0134370.
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PR 18-MAY-1999; 99US-0134941.
PR 19-MAY-1999; 99US-0134941.
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PR 08-JUN-1999; 99US-0138094.
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PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.

PR	06-AUG-1999;	99US-0147303.
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PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152353.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154039.
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PR	24-SEP-1999;	99US-0156559.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
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PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
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PR	22-OCT-1999;	99US-0160989.
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PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match	23.9%;	Score 419.5;	DB 21;	Length 307;
Best Local Similarity	35.7%;	Pred. No. 2.1e-37;		

Matches	107;	Conservative	57;	Mismatches	101;	Indels	35;	Gaps	7;
QY	55	EHERNFVPGFEYLSRFQSRSLDANARESVGILKAVYGFQPLTAYLAVMYMDRFLDS	114						
DB	16	ENETNPGCFQIILDFL-----VSCREALDWLRYKXSHGFTSLAALAVNFDKPMIS	70						
QY	115	RLPETHGWLQVSVACSLAKMEPLVPSLIDQIEBAKITEPRTRRELLVIGV	174						
DB	71	IKLQTRPMQSVLVNVAISLAKVEIQVPLLDIDVEARVILFEAKTIORRELLIST	130						
QY	175	LDWRLRSVPLCF---LAFACKVDSTGTFFIRPLSRATEIIVSNQESFLAYPSCI	230						
DB	131	LQWRMHVPTISPFDDIIRFGSKHQQLDFCR---KCRLLISVADTRFRFPSPVL	186						
QY	231	AAAIITLANEIPMWSVYKPEENASWCEGLRKEKVGICYOIMQELVINNRRLPLKYL	290						
DB	187	ATAIMILVEELKRCDEVERVQSQTTLKVNQEKVNCY---ELLEHNPSKRRMNLV	242						
QY	291	PQ-----LRYTTRIRMSSTVYSSFSSSSTFSLSCKRRLLN-----NRLWD	333						
DB	243	DQSPSGVLDFDDSSNSMWSVSTTASVSSSSSSEPEL-LKRRVQEQMLPSINRMFLD	301						

RESULT 12	
AAAG23946	
ID	AAAG23946 standard; Protein; 367 AA.
AC	AAAG23946;
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 27438.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
XX	
OS	Arabidopsis thaliana.
PN	EP1033405-A2.
PD	06-SEP-2000.
XX	
PE	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
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PR	06-APR-1999; 99US-0128234.
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PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.
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PR	04-MAY-1999; 99US-0132484.
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PR 26-AUG-1999; 99US-0150884.
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PR 15-SEP-1999; 99US-0154018.
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PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
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QY 118 PETNGPQLVSVACLSLAKMEPPLVPSJDDIQLEGAKYLFEPKTRKMEELLVLSVDDM 177

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AC AAG07075;

DT	17-OCT-2000 (first entry)
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DE	Arabidopsis thaliana protein fragment SEQ ID NO: 4088.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter
KW termination sequence.

OS *Arabidopsis thaliana*.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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AC AAG53864;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 66617.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EPI033405-A2.

PD 06-SEP-2000.

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 14:36:49 ; Search time 18 Seconds

(without alignments)
1809.682 Million cell updates/sec

Title: US-09-665-308D-12

Sequence: 1 MSVSCSLSDYDLGCEDESSGI.....SCKRRKLNRLNWDKXNSE 339

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Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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1: PIR.71.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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29	198.5	11.3	491	2	S14166

30	197.5	11.2	454	2	S16522	mitosis-specific c
31	197	11.2	449	2	S49904	cyclin - common to
32	197	11.2	460	2	B86339	protein F2D10.10 f
33	196.5	11.2	341	2	S16521	mitosis-specific c
34	196.5	11.2	419	2	T03675	cyclin 2 - rice
35	196.5	11.2	471	2	S14165	cyclin B1 - yeast
36	196	11.1	398	2	T12330	hypothetical prote
37	195.5	11.1	493	2	T03609	cyclin, A-type - c
38	194.5	11.0	473	2	S41709	mitosis-specific c
39	193.5	11.0	446	2	T03021	mitosis-specific c
40	192	10.9	484	2	T07675	cyclin a2-type, m
41	191.5	10.9	415	2	T51637	cyclin a2 - Africa
42	191	10.9	460	2	D96505	probable mitotic c
43	190	10.8	398	2	S21529	cyclin B2 - mouse
44	190	10.8	399	2	S23596	cyclin B2 - chick
45	189.5	10.8	408	2	S17793	cyclin B - common

ALIGNMENTS

RESULT 1

A96725
hypothetical protein F20P5.7 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A96725

R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulster, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Matli, R.; Marzia, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: A96725

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-339 <STO>

A:Cross-references: GB:AE005173; NID:g2194121; PIDN:AB61096.1; GSPDB:GN00141

C:Genetics:

A:Gene: F20P5.7

A:Map position: 1

Query Match 58.6% Score 1030; DB 2; Length 339;

Best local similarity 63.3% Pred. No. 4.1e-85;

Matches 214; Conservative 44; Mismatches 62; Indels 18; Gaps 7;

QY	1	MSVSCSLSDYDLGCEDESSGILSGESP-ECSFSDIDSSPPPTEDCSTASFIEHRN	59
DB	12	MSVSCSLSDYDLGCEDESSGILSGESP-ECSFSDIDSSPPPTEDCSTASFIEHRN	61
QY	60	FVFGFEFLSRFGSRSDAANARESVGMILKVAAYGFOGLTAYLVANVMDRFLDRRLP	119
DB	62	FVFGFEFLSRFGSRSDAANARESVGMILKVAAYGFOGLTAYLVANVMDRFLDRRLP	121
QY	120	TGMPMQLAVLACTSLAAKKEETLVPSLDFQVAGVKYLFKAKTIKRMELTAVLDWRL	181
DB	122	TGMPMQLAVLACTSLAAKKEETLVPSLDFQVAGVKYLFKAKTIKRMELTAVLDWRL	181
QY	180	RSVTPPELFAFAKQVDSGTGTFRLFLISRATETIVSNIOEAFVAVMPSCIAAAILTRA	239
DB	182	RSVTPPELFAFAKQVDSGTGTFRLFLISRATETIVSNIOEAFVAVMPSCIAAAILTRA	241
QY	240	NEIPNM-SVVKP-ENAESMCEGLRKEKVGICVQAMQELVNNORPLPLKLYLPOLRYTT	297
DB	242	NEIPNM-SVVKP-ENAESMCEGLRKEKVGICVQAMQELVNNORPLPLKLYLPOLRYTT	299
QY	298	RTMRSSIVSSFSSSSTFSLSCSKRRKLNRLNWDKXNSE	335
DB	299	RTMRSSIVSSFSSSSTFSLSCSKRRKLNRLNWDKXNSE	335

Db 300 RA---SSTLRPSDESSFSSSSPCKRRRLSGYSWVGDE 334

RESULT 2

S51650

cyclin delta-1 - Arabidopsis thaliana

N;Alternate names: cyclin D homolog

C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Sep-1997

C;Accession: S51650

R;Soni, R.; Carmichael, J.P.; Shah, Z.H.; Murray, J.A.H.

submitted to the EMBL Data Library, December 1994

A;Description: A family of cyclin D homologs from plants differentially controlled by gr

A;Reference number: S51650

A;Accession: S51650

A;Molecule type: mRNA

A;Residues: 1-334 <SON>

A;Cross-references: EMBL:X83369; NID:9603504; PID:9603505

C;Keywords: cell cycle control; cell division control

Query Match

Best Local Similarity 54.0%; Score 949.5; DB 2; Length 334;

Matches 204; Conservative 44; Mismatches 67; Indels 23; Gaps 9;

Db 1 MSVSCSLDYDLGDSGSGILSGSP-ECSPSIDSSPPSPPTEDCYSIASFIEHERN 59

Db 12 MSVSFNDMDLFCEGD-SGVFSGESTVDFSSSEVDMPGD-----SIACFIEDERT 61

Qy 60 FVPGFEYLSRQSRSLDANAREESGWLTKYHAYGPOPLAYLVNMDREFLSRLPE 119

Db 62 FVPGHDYLSRQSRSLDANAREESGWLTKYHAYGPOPLAYLVNMDREFLSRLPE 121

Qy 120 TNGWMLQVAVACSLAKMKEEPLVPSLLDQIEGAKTFFPRTRRMELLVGLDMRL 179

Db 122 TSGWMLQVAVACSLAKMKEEPLVPSLLDQIEGAKTFFPRTRRMELLVGLDMRL 181

Qy 180 RSVTPPLCLAFPAACKVDSTGTFIRPLISRATETIIVNQESFLAYWPCSTAAAILTAA 239

Db 182 RSVTPPLCLAFPAACKVDSTGTFIRPLISRATETIIVNQESFLAYWPCSTAAAILTAA 240

Qy 240 NEIRPW-GVVP-ENAESGELREKRYIGCYQMOELVINNNOKPLVLVLQRLRTT 297

Db 241 NEIRPW-GVVP-ENAESGELREKRYIGCYQMOELVINNNOKPLVLVLQRLRTT 298

Qy 298 RTRMRSTVSSFSSTSSSTFSCSKRRRLNNRLWYDCK 335

Db 299 RA---SSTLRPSDESSFS---PCKRRRLSGYSWVGDE 329

RESULT 3

T09961

cyclin D-like protein - red goosefoot

C;Species: Chenopodium rubrum (red goosefoot)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: T09961

R;Renz, A.; Fountain, M.; Beck, E.

submitted to the EMBL Data Library, December 1996

A;Description: Nucleotide sequence of a cDNA encoding a D-type cyclin from a photoautot

A;Reference number: Z16906

A;Accession: T09961

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-372 <RND>

A;Cross-references: EMBL:Y10162; NID:61014005; PID:e290219

A;Experimental source: 7 day old culture; photoautotrophic cells derived from hypocotyl

C;Genetics:

A;Gene: cycD1

C;Keywords: cell cycle control; cell division control

Query Match

Best Local Similarity 26.4%; Score 463.5; DB 2; Length 372;

Matches 120; Conservative 66; Mismatches 116; Indels 77; Gaps 9;

Qy 9 YDLGCGDSGILSGSPESFSDIDSSPPSPPTEDCYSI----- 50

Db 5 FDLGCAEDNSI-----FDEVDDN--YGVVDDDLQICNQQOQHGNLRNFDFTL 53

Qy 51 -----ASFIEHERNFVPEFELSLFQSRSLDANAREESV 84

Db 54 ILLIIRKHNFEALISGFVAVNHECLASLEDFRHLGLDLKRRFGDLDLGRNLVI 113

Qy 85 GWLTKYHAYGPOPLAYLVNMDREFLSRLPEPTNGWMLQVAVACSLAKMKEEPLV 144

Db 114 DWLHKQSHNREFPLCYLVSVNIDREFLSRLPE-GKAMMQLLVACSLAKMKEEPLV 172

Qy 145 PSLLDQIEGAKTFFPRTRRMELLVGLDMRLRSVTPPLCLAFPAACKVDSTGTFIR 204

Db 173 PLIIDLQVSEKRFVFAKTQIRMEELLVSTLTKRMQSVTFEFDYFLTKLSGDMPSKS 232

Qy 205 LISRAETIIVNQESFLAYWPCSTAAAILTANETIIVNQESFLAYWPCSTAAAIL 262

Db 233 LIQQAQLILSTKIGIDLEFPESEIAAVASIVQOT--OIVETDAFSEFLTDHEK 289

Qy 263 EKVIGCYQMOELVINNNOKPLVLVLQRLRTTRMRSTVSSFSSTSSSTFSLC- 321

Db 290 ERLMKVEIMHDLRMSRSRGALASTVQSPVIGVLD--ASACLKYSDDSTTTPSGSGC 347

Qy 322 -----KRRKLN 327

Db 348 NSAHSSPASAPAPKRRKLD 366

RESULT 4

C84613

probable cyclin D (imported) - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cross)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: C84613

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Motilal, K.S.; Cronin, L.A.; Shen, M.; Yanakiev, S.E.; Umayan, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; M0ID:20083487

A;Accession: C84613

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-361 <STO>

A;Cross-references: GB:AE002093; NID:94544444; PIDN:AAD2352.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g2490

A;Map position: 2

Query Match

Best Local Similarity 25.7%; Score 451; DB 2; Length 361;

Matches 120; Conservative 60; Mismatches 120; Indels 48; Gaps 9;

Qy 10 DLGCGDSGILSGSPESFSDIDSSPPSPPTEDCYSI-----SSP---PPSPPT 44

Db 4 NLACGETSESWIIDNDDDIDNYGGFTNEIDYHQLFANDQFNGSGSLPMKSSSSSLS 63

Qy 45 EDCYSIASFIEHERNFVPEFELSLFQSRSLDANAREESGWLTKYHAYGPOPLAYLA 104

Db 64 ED-RIKEMLVRELFEFGTDIVYKRLISGDLISYRNQALDWLTKCAHYHGHCLTICS 121

Qy 105 VYVMDREFLSRLPEPTNGWMLQVAVACSLAKMKEEPLVPSLLDQIEGAKTFFPR 164

Db 122 MNYVMDREFLSRLPEPTNGWMLQVAVACSLAKMKEEPLVPSLLDQIEGAKTFFPR 181

Qy 165 RMWELVGLVDMRLRSVTPPLCLAFPAACKVDSTGTFIRPLISRATETIIVNQES 224

Db 182 RMWELVGLVDMRLRSVTPPLCLAFPAACKVDSTGTFIRPLISRATETIIVNQES 239

Qy 225 YWPCSTAAAILTANETIIVNQESFLAYWPCSTAAAILTANETIIVNQESFLAY 284

Db 240 FRPEIAAAAVSIS-GETECTIDEKALSLIYVQKRWKRLNMSLAGEENVKGT 298

QY 285 PULKYLPLRYVTRT-----RMSSTVSSSSSSSS 316
 Db 299 SLQ--EQARVAVRVPASPVLNATCLSRSEERTVESCTNSOSS 344

RESULT 5

551651
 cyclin delta-2 - Arabidopsis thaliana
 N:Alternate names: cyclin D homolog
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 25-Apr-1997
 R:Submitted to the EMBL Data Library, December 1994
 A:Description: A family of cyclin D homologs from plants differentially controlled by gr
 A:Accession: S51651
 A:Accession: S51651
 A:Molecule type: mRNA
 A:Residues: 1-383 <SON>
 A:Cross-references: EMBL:X83370
 C:Keywords: cell cycle control; cell division control

Query Match 25.3%; Score 444; DB 2; Length 383;
 Best Local Similarity 35.4%; Pred. No. 3.7e-32;
 Matches 115; Conservative 57; Mismatches 121; Indels 32; Gaps 7;

QY 8 DYDLGDSGSLSGSPESFSDIDSSPPPTTEDCSIASFIEHENFVPGPEYL 67
 Db 36 NHOIAKADNFG-GNGSIPMGSSS-----SLSD-RIKEMVRELTEFCPGDYV 84
 QY 68 SFQSRSLDANARESVGMILKVAHYGFQPLTAYLVAVMYDRFLDSRRLPETNGMPLQ 127
 Db 85 KRLISGDIPLSVNQAQMLKVCANHYHFGHICLSNVDRLFTSVELPKDQMAQL 144
 QY 128 VSVACLSIAAKMEPLVSLDQIGAKYIFEPRTIRRMELLYGLVDMRLSVTLPLCF 187
 Db 145 LAVSCLSLASKMEETDVHIDVLEDPFVEAKTIKRMELVVTLLNRLQLTPEFSF 204
 QY 188 LAFFACKVDSGTGTFIRFLISRATEIIVSNIOEASFIAWPSICIAAAILTPANRIPMVS 247
 Db 205 IDYFADKI--SGHSENLIIYSSSRILNTTAKIEFLDRPEIILAAAVSYSTIS-GETEC 261
 QY 248 VAPNAESWCBGLREKVIYGYQLMQLVIVNNQRKLPPLKVLDPOLVTRT----- 299
 Db 262 IDEERKALSLIYKQERVKRLINLRSLTGEENVGTSLQ--EQARVAVRVPASPVL 319
 QY 300 -----RMSSTVSSSSSSSS 316
 Db 320 LEATCLSTRSEERTVESCTNSOSS 344

RESULT 6

705420
 cyclin delta-3 - Arabidopsis thaliana
 N:Alternate names: cyclin D homolog; protein F28A23.80
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
 C:Accession: T05420; S51652
 R:Submitted to the EMBL Data Library, December 1994
 A:Description: A family of cyclin D homologs from plants differentially controlled by gr
 A:Accession: T05420
 A:Accession: S51652
 A:Molecule type: DNA
 A:Residues: 1-376 <BEV>
 A:Cross-references: EMBL:AL021961
 A:Experimental source: cultivar Columbia; BAC clone F28A23
 R:Submitted to the EMBL Data Library, December 1994
 A:Description: A family of cyclin D homologs from plants differentially controlled by gr
 A:Accession: S51652
 A:Molecule type: mRNA

A:Residues: 1-287, 'C', 289-370, 'R', 372-376 <SON>
 A:Cross-references: EMBL:X83371; NID:9603508; P1D:9603509
 C:Genetics:
 A:Map position: 4
 A:Introns: 158/3; 226/1; 269/3
 A:Note: F28A23.80
 C:Keywords: cell cycle control; cell division control

Query Match 23.7%; Score 416; DB 2; Length 376;
 Best Local Similarity 32.9%; Pred. No. 1.2e-29;
 Matches 105; Conservative 58; Mismatches 124; Indels 32; Gaps 5;

QY 10 DLGCDSSGSLSGSPESFSDIDSSPPPTTEDCSIASFIEHENFVPGPEYL 64
 Db 20 DMLYCEERKWDGEVE-ENSSLSPPVYVLOQDLFWEDDLVTLFSEKESGLSCL 78
 QY 65 E-VYSRFSRLDANARESVGMILKVAHYGFQPLTAYLVAVMYDRFLDSRRLPETNG 122
 Db 79 DQVYLS-----TDREAVGWLIRVNAHGFSTLAVALITYLDKFICTSLQDKP 129
 QY 123 WPLQVSVACLSIAAKMEPLVSLDQIGAKYIFEPRTIRRMELLYGLVDMRLSV 182
 Db 130 WMLQVSVACLSIAAKMEPLVSLDQIGAKYIFEPRTIRRMELLYGLVDMRLSV 189
 QY 183 TPLCFIAFACKVDSGTGTFIRFLISRATEIIVSNIOEASFIAWPSICIAAAILTPANEI 242
 Db 190 TPLSFVDHIIIRLGLKNNAMFCLKHRLISVSDRFPGLVPSVAAATMGRITEQV 249
 QY 243 PMSVVKPBNASWCBGLREKVIYGYQLMQLVIVNNQRKLPPLKVLDPOLVTRT 302
 Db 250 DPEFPLSYOTNLIAGVNLTKREKVCYDILQLPVD-----RIGLQIQIQ 294
 QY 303 SSVVSSSSSSSSS 321
 Db 295 SKRKRSHDSSSSLSNPSC 313

RESULT 7

T45860
 cyclin D3-like protein - Arabidopsis thaliana
 N:Alternate names: protein F3A4.150
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C:Accession: T45860
 R:Submitted to the EMBL Data Library, December 1999
 A:Description: A family of cyclin D homologs from plants differentially controlled by gr
 A:Accession: T45860
 A:Accession: T45860
 A:Molecule type: DNA
 A:Residues: 1-361 <BAR>
 A:Cross-references: EMBL:AL132978
 A:Experimental source: cultivar Columbia; BAC clone F3A4
 C:Genetics:
 A:Map position: 3
 A:Introns: 157/3; 225/1; 268/3
 A:Note: F3A4.150

Query Match 23.4%; Score 411; DB 2; Length 361;
 Best Local Similarity 31.4%; Pred. No. 3.2e-29;
 Matches 109; Conservative 59; Mismatches 119; Indels 60; Gaps 7;

QY 6 LSDYDLGDSGSLSGSPESFSDIDSSPPPTTEDCSIASFIEHENFVPGPEYL 65
 Db 49 LSDHDMIMDDDELSTLSKQEPCLYDEL-----LDD-----E 80
 QY 66 YLSRFSRLDANARESVGMILKVAHYGFQPLTAYLVAVMYDRFLDSRRLPETNGMPL 125
 Db 81 FL-----VLCREKALDMLFKVSKSHGPNLSLALAVNFDFTLSKRFQTDKPMWS 131
 QY 126 QLVSVACLSIAAKMEPLVSLDQIGAKYIFEPRTIRRMELLYGLVDMRLSV 185
 Db 132 QLTALACLSIAAKMEPLVSLDQIGAKYIFEPRTIRRMELLYGLVDMRLSV 191

QY 186 CELAFACKVDSTGTFFIRFLISRAETELIVSNIQESFLAWPSCIAAAAILTAAETPNW 245
 Db 192 SFEDHIIIRYSPKSHQLEFLSRCESLILIPDSRFLSPSVLAIAIMVSYRDLKMC 251
 QY 246 SYVKEENNAESMCEGLRKEKVGICVOLMOELVYINNORLPLLLKVLPO---LRTYTRRM 301
 Db 252 DEAYVOSOLMTLLKVDKSRKNCY---ELVLDHSPSKRRKMMNQOPASPIGVFADSPS 307
 QY 302 RSSVTSFSSSSSTSTFSLS-----CKRRKLN-----NRLWVD 333
 Db 308 SSSSMESWVVSASASVSSSPSEPEPLKKRRRVQEQOQMLSLINRMFFD 354

RESULT 8 T49995

cyclin protein-like - Arabidopsis thaliana
 N:Alternate names: protein F12B17.210
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
 C:Accession: T49995
 R:Bayan, M.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: 225026
 A:Accession: T49995
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-317 <BEV>
 A:Cross-references: EMBL:AL353995; GSPDB:GN00063; ATSP:F12B17.210
 A:Experimental source: cultivar Columbia; BAC clone F12B17
 C:Genetics:
 A:Gene: ATSP:F12B17.210
 A:Map position: 5
 A:introns: 78/3; 107/3; 140/3; 221/3; 266/3

Query Match 20.9%; Score 368; DB 2; Length 317;
 Best Local Similarity 35.5%; Pred. No. 2.1e-25;
 Matches 104; Conservative 47; Mismatches 104; Indels 38; Gaps 8;

QY 50 IASFTIEHNEVPGFEYLSRFQSRSLDANAREESVGMILKHAHYGFQPLATVAVNMD 109
 Db 39 VRMEIEKEHQSPRDYDLKRLKNGDLDFNVRIQALGWTMKACEELQFGPLICIAMNVL 98
 QY 110 RFLDSRLPETNGWPLQVSVACLSIAAKMEPLVPSLLDQIEGAKTIEPRTIRREL 169
 Db 99 RFLSVNDLDSGKAWYQVLAACLSIAKIEETINPELMQLOVGAPMVFEKKSQRMEL 158
 QY 170 LVLGVLDWRLRSVTPPLCFAPACKVDSTGTPIRE-LISRAETIVSNIQ----- 218
 Db 159 LVLMVLRMLRAVTPCSYVRYFLSKINGYDQPHSRILVTRSLQVIASTKGDRLGLFFPK 218
 QY 219 -----EASFLAWPSCIAAAAILTAAET-IPNMSVYKPEENNAESMCEGLRKEV--I 266
 Db 219 GVLIVDVMAGIDFLERRASEIAAVALSVSGEHFDKFSF-----SSFSLSLEKERVAKI 272
 QY 267 GCYQLMOELVYINNORLPLKVLQPLRVTRTMRSSVSSFS-SSSTSTPS 318
 Db 273 G---EKIERDSSSSSQGTNNVYL-----QFKSRKYSLSLSTAVSSSLTSLIS 317

RESULT 9 T09598

cyclin 4, D-type - alfalfa
 C:Species: Medicago sativa (alfalfa)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T09598
 R:Dahl, M.; Meskiane, I.; Boegre, L.
 Plant Cell 7, 1847-1857, 1995
 A:Title: The D-type alfalfa cyclin gene cymc4 complements G1 cyclin-deficient yeast and
 A:Reference number: 216760; MIM:96093424
 A:Accession: T09598
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-386 <DAH>
 A:Cross-references: EMBL:X88864; NID:g1150931; PIDN:CAA61334.1; PID:g1150932
 C:Genetics:
 A:Note: cymc4

Query Match 20.9%; Score 367; DB 2; Length 386;
 Best Local Similarity 37.7%; Pred. No. 3.3e-25;
 Matches 90; Conservative 40; Mismatches 81; Indels 28; Gaps 6;

QY 52 SFIEHNEVPGFEYLSRFQSRSLDANAREESVGMILKHAHYGFQPLATVAVNMDR 111
 Db 92 TYVEDLKNI-NDLSLQ-----PRRAVEMLKVNHYGSALTATLAVNYLDRE 141
 QY 112 LDSRLPETNGWPLQVSVACLSIAAKMEPLVPSLLDQIEGAKTIEPRTIRREL 171
 Db 142 LLSFHQKRPKPMIQLVAVTCISLAKVETQVPLLDQVQDTKYVEARTIQMELLI 201
 QY 172 LGVLDWRLRSVTPPLCFAP---FACKVDSTGTFFIRFLISRAETIVSNIQESFLAWP 227
 Db 202 LSLTKMKMHPVTHSLDITIRLGLKTYLHMEFLR---KENLLSLVLDSSRVGCV 257
 QY 228 SCIAAAAILTAAETIPNMSVYKPEENNAESMCEGL-----RKEVIGCYQLMOELVINNN 280
 Db 258 SVLATATVMTLHVLDIQIQQ---SDPNGVDYKQGLNVLAKISKREKVECYNAIHLTNANN 312

RESULT 10 E85041

probable D-type cyclin [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C:Accession: E85041
 R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: A85001; MIM:20083488
 A:Accession: E85041
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-302 <STO>
 A:Cross-references: GB:NC_001268; NID:g7270197; PIDN:CAB77812.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: AT4G03270
 A:Map position: 4

Query Match 19.4%; Score 340.5; DB 2; Length 302;
 Best Local Similarity 32.5%; Pred. No. 5.9e-23;
 Matches 93; Conservative 54; Mismatches 106; Indels 33; Gaps 9;

QY 57 ERNFVPGFEYLSRFQSRSLDANAREESVGMILKHAHYGFQPLATVAVNMDRFLDSRR 116
 Db 35 EPOHMPSSHFHSLKSAFLSNRQALISITQYSKRP-DSLTIVLAVNYDRLSSED 93
 QY 117 LPETNGWPLQVSVACLSIAAKMEPLVPSLLDQIEGAKTIEPRTIRRELVLGVLD 176
 Db 94 MPOSKPILKLISLSCVSIKAKRKPM-SSVSLPEGE--PEDQMIERMEVILGLAK 150
 QY 177 WRLRSVTPPLCFAP---FACKVDSTGTFFIRFLISRAETIVSNIQESFLAWPSCIAA 232
 Db 151 WRMSVTPFSFLAFSLFELKEDPLLLKHSLSKTSQSLDLSLDFLSEKFSVLAG 210
 QY 233 AAILTAAET-----PNMSVYKPEENNAESMCEGLRKEKVGICVOLMOE-LVINNORLPL 285
 Db 211 AAILFASFLCPLQFQFS-----NRINQCTYNNKQELMECKAIQERDRIIYGENEGS-- 263
 QY 286 LKAVLPQLVTRTMRSSVSSFSSSSTSF--SLSCRRKLNNR 329
 Db 264 -----TETAVNVLDQFSSCESDKSITITVASSPPRRRTSR 300

RESULT 11 T04720

hypothetical protein F19F18.120 - Arabidopsis thaliana

14.18; Score 247; DB 2; Length 454;

180 VTSYTFSGTLNSKIGMGD--HMIMNRITNHLDVLCDLKLOPPSVATAAI----- 231

NO	DATE	DESCRIPTION	AMOUNT
1	1980-01-01	INITIAL DEPOSIT	1000.00
2	1980-02-15	WITHDRAWAL	50.00
3	1980-03-10	DEPOSIT	250.00
4	1980-04-20	WITHDRAWAL	120.00
5	1980-05-05	DEPOSIT	75.00
6	1980-06-18	WITHDRAWAL	30.00
7	1980-07-01	DEPOSIT	150.00
8	1980-08-12	WITHDRAWAL	80.00
9	1980-09-25	DEPOSIT	200.00
10	1980-10-10	WITHDRAWAL	40.00
11	1980-11-30	DEPOSIT	100.00
12	1980-12-15	WITHDRAWAL	60.00
13	1981-01-01	DEPOSIT	180.00
14	1981-02-20	WITHDRAWAL	90.00
15	1981-03-10	DEPOSIT	110.00
16	1981-04-05	WITHDRAWAL	55.00
17	1981-05-15	DEPOSIT	130.00
18	1981-06-25	WITHDRAWAL	70.00
19	1981-07-10	DEPOSIT	160.00
20	1981-08-20	WITHDRAWAL	85.00
21	1981-09-05	DEPOSIT	190.00
22	1981-10-15	WITHDRAWAL	45.00
23	1981-11-25	DEPOSIT	120.00
24	1981-12-10	WITHDRAWAL	65.00
25	1982-01-01	DEPOSIT	170.00
26	1982-02-15	WITHDRAWAL	95.00
27	1982-03-10	DEPOSIT	140.00
28	1982-04-05	WITHDRAWAL	75.00
29	1982-05-15	DEPOSIT	155.00
30	1982-06-25	WITHDRAWAL	80.00
31	1982-07-10	DEPOSIT	185.00
32	1982-08-20	WITHDRAWAL	90.00
33	1982-09-05	DEPOSIT	165.00
34	1982-10-15	WITHDRAWAL	50.00
35	1982-11-25	DEPOSIT	135.00
36	1982-12-10	WITHDRAWAL	70.00
37	1983-01-01	DEPOSIT	195.00
38	1983-02-15	WITHDRAWAL	100.00
39	1983-03-10	DEPOSIT	175.00
40	1983-04-05	WITHDRAWAL	85.00
41	1983-05-15	DEPOSIT	160.00
42	1983-06-25	WITHDRAWAL	95.00
43	1983-07-10	DEPOSIT	180.00
44	1983-08-20	WITHDRAWAL	105.00
45	1983-09-05	DEPOSIT	190.00
46	1983-10-15	WITHDRAWAL	110.00
47	1983-11-25	DEPOSIT	200.00
48	1983-12-10	WITHDRAWAL	115.00
49	1984-01-01	DEPOSIT	210.00
50	1984-02-15	WITHDRAWAL	120.00
51	1984-03-10	DEPOSIT	220.00
52	1984-04-05	WITHDRAWAL	125.00
53	1984-05-15	DEPOSIT	230.00
54	1984-06-25	WITHDRAWAL	130.00
55	1984-07-10	DEPOSIT	240.00
56	1984-08-20	WITHDRAWAL	135.00
57	1984-09-05	DEPOSIT	250.00
58	1984-10-15	WITHDRAWAL	140.00
59	1984-11-25	DEPOSIT	260.00
60	1984-12-10	WITHDRAWAL	145.00
61	1985-01-01	DEPOSIT	270.00
62	1985-02-15	WITHDRAWAL	150.00
63	1985-03-10	DEPOSIT	280.00
64	1985-04-05	WITHDRAWAL	155.00
65	1985-05-15	DEPOSIT	290.00
66	1985-06-25	WITHDRAWAL	160.00
67	1985-07-10	DEPOSIT	300.00
68	1985-08-20	WITHDRAWAL	165.00
69	1985-09-05	DEPOSIT	310.00
70	1985-10-15	WITHDRAWAL	170.00
71	1985-11-25	DEPOSIT	320.00
72	1985-12-10	WITHDRAWAL	175.00
73	1986-01-01	DEPOSIT	330.00
74	1986-02-15	WITHDRAWAL	180.00
75	1986-03-10	DEPOSIT	340.00
76	1986-04-05	WITHDRAWAL	185.00
77	1986-05-15	DEPOSIT	350.00
78	1986-06-25	WITHDRAWAL	190.00
79	1986-07-10	DEPOSIT	360.00

Db 232 ---WIMEDKVCRESIMNLFQDNHKEKIVKCYDGNKNDIDHSSR 274

RESULT 14

T02746

Cyclin A-like protein CYCZM2W - maize

C:Species: Zea mays (maize)

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Jul-1999

C:Accession: T02746

R:Heien, W.L.; Molnár, S.M.

Plant Mol. Biol. 37, 121-129, 1998

A:Title: Isolation and characterization of a functional A-type cyclin from maize.

A:Reference number: 214713; MID:98281580

A:Accession: T02746

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1502 <HS>

A:Cross-references: EMBL:U50064; NID:g1399509; PIDN:AA050013.1; PID:g1399510

A:Experimental source: cultivar Merit; root tip

C:Genetics:

A:Gene: CYCZM2W

C:Superfamily: cyclin

Query Match 13.0%; Score 228; DB 2; Length 502;

Best Local Similarity 29.2%; Pred. No. 16-12;

Matches 77; Conservative 42; Mismatches 103; Indels 42; Gaps 10;

QY 29 SFSDISSPPPTTEDCYSIAFI-----EHERNFVPGFEYLSRFQSRSLDANAREES 83

Db 217 SICEVDNPFEDP---QLCAALASDIYMHLEEMKRRPSTDMETIQ-KDVNFSMRAIL 271

QY 84 VGLIKYHAYYGQPLAVIYAVNYMDRFLDSRRPLPTNGMPLOLVAVACLISIAKMEEP 143

Db 272 IDMLVEVAEETRLAPDLITLVNIDRYLSGN---EINRQLDLGVACMLIAKYEETIC 328

QY 144 VPSLDQIGAKYIEPRTIR---RMELLYGVLDWRLRSVTPCLAF-----ACK 194

Db 329 AP-----QVEEFCYTDNIFYRDEVLDMESVLYLKFEMTAPTKCFRRFARSAQACD 383

QY 195 VDSGTFRPLISRAETIIVSNIOEASFLAYWPCIAAAAILTAA-----NEIP 243

Db 384 ED-PAHLEFLANIYAEI---SLEYSLSYSPSLIAASIFLAFVLOPTKYPWNSTLA 439

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 244 NMSVKKPENASWCEGLRKEKVI 267

Db 440 HTQYKPSLSECVKALHRLSVG 463

QY 87 ILKHYAYGQPLAVIYAVNYMDRFLDSRRPLPTNGMPLOLVAVACLISIAKMEEP 146

Db 226 LVEVAEETRLAPDLITLVNIDRYLSGNIEIRRR---QLDLGVACMLIAKYEETIC 281

QY 147 LLDQIGAKYIEPRTIR---RMELLYGVLDWRLRSVTPCLAF-----ACKYDS 197

Db 282 ---QVEEFCYTDNIFYRDEVLDMESVLYLKFEMTAPTKCFRRFARSAQACD- 336

QY 198 TGTFRPLISRAETIIVSNIOEASFLAYWPCIAAAAILTAA-----NEIPNWS 246

Db 337 PALHLEFLANIYAEI---SLEYSLSYSPSLIAASIFLAFVLOPTKYPWNSTLAHYT 393

QY 247 VVKPENASWCEGLRKEKVI 288

Db 394 QYKP-----SKLSECVKALHRLCSVSGSNLPAIR 423

Search completed: October 23, 2002, 14:39:31

Job time : 19 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 23, 2002, 14:34:34 : Search time 14 Seconds

(without alignments)
937.566 Million cell updates/sec

Title: US-09-665-308D-12

Perfect score: 1758

Sequence: 1 MSVSCLSDDYLLCGEDSSGI.....SCKRRKLNLMVDDKGNSE 339

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1017	57.8	335 1 CGD1_ARATH	P42751 arabidopsis
2	451	25.7	361 1 CGD2_ARATH	P42752 arabidopsis
3	417	23.7	376 1 CGD3_ARATH	P42753 arabidopsis
4	205.5	11.7	441 1 CG22_ANTWA	P34801 antirrhinum
5	201	11.4	397 1 CGB2_MESAU	P37883 mesocricetu
6	200	11.4	328 1 CGB2_MESAU	P30278 medicago sa
7	200	11.4	434 1 CGB2_MESAU	P46278 medicago va
8	199	11.3	428 1 CGB2_ARATH	P30183 arabidopsis
9	198.5	11.3	491 1 CG22_YEAST	P24869 saccharomyc
10	197.5	11.2	454 1 CG21_SOYBN	P25011 glycyne max
11	196.5	11.2	341 1 CG2A_DAUCA	P25010 dancus caro
12	196.5	11.2	419 1 CG2B_ORYSA	P40671 oryza sativ
13	196.5	11.2	471 1 CG21_YEAST	P24868 saccharomyc
14	196	11.1	398 1 CGB2_HUMAN	P34800 antirrhinum
15	194.5	11.1	473 1 CG21_ANTWA	P47800 antirrhinum
16	191.5	10.9	415 1 CGA2_XENLA	P47827 xenopus lae
17	190	10.8	398 1 CGB2_MOUSE	P30332 gallus galli
18	190	10.8	399 1 CGB2_CHICK	P24862 patella vul
19	189.5	10.8	408 1 CGB2_PATVU	P42777 medicago va
20	189	10.8	426 1 CG1B_MEDVA	P42861 patella vul
21	188.5	10.7	426 1 CGB2_PATVU	P42861 patella vul
22	187.5	10.7	291 1 CGD1_BRARE	O90459 brachydanio
23	187	10.6	398 1 CGB2_BOVIN	O77689 bos taurus
24	185.5	10.6	257 1 CG22_SOYBN	P35012 glycyne max
25	184.5	10.5	430 1 CGB1_MOUSE	P24860 mus musculu
26	183	10.4	291 1 CGD2_XENLA	P37882 xenopus lae
27	182.5	10.4	422 1 CGA2_MOUSE	P31943 mus musculu
28	182.5	10.4	432 1 CGA2_HUMAN	P30248 homo sapien
29	181.5	10.3	406 1 CGA2_BOVIN	P30274 bos taurus
30	180.5	10.3	409 1 CGB2_ARABU	P07818 arabacia pun
31	180.5	10.3	423 1 CGB1_RAT	P30277 rattus norv
32	180	10.2	397 1 CGB1_XENLA	P31350 xenopus lae
33	179.5	10.2	291 1 CGD1_XENLA	P30755 xenopus lae

34	179.5	10.2	392 1 CGB2_XENLA	P13351 xenopus lae
35	179	10.2	395 1 CGA2_CHICK	P43449 gallus galli
36	178.5	10.2	289 1 CGD2_MOUSE	P30280 mus musculu
37	177.5	10.1	288 1 CGB2_RAT	P04827 rattus norv
38	177.5	10.1	421 1 CGA2_MESAU	P37881 mesocricetu
39	176.5	10.0	289 1 CGD2_HUMAN	P30279 homo sapien
40	176.5	10.0	482 1 CG23_SCHPO	P10815 schizosacch
41	176	10.0	421 1 CGA1_MOUSE	P61456 mus musculu
42	175	10.0	295 1 CGD1_RAT	P39948 rattus norv
43	175	10.0	420 1 CG2A_CHLVR	P51966 chlorohydra
44	174.5	9.9	380 1 CGS6_YEAST	P32943 saccharomyc
45	174.5	9.9	429 1 CGB1_CRILLO	O08301 cricetus

ALIGNMENTS

RESULT 1
ID CGD1_ARATH STANDARD: PRT; 335 AA.
AC P42751: 004525;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cyclin delta-1.
GN CYCLD OR AT1G70210 OR F20P5.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
ON NCBI_Taxid=3702;
[1]
RX SEQUENCE FROM N.A.
RC STRAIN=CV, LANDSBERG ERECTA; TISUP=Seedling;
RX MEDLINE=95210930; PubMed=7696881;
RA Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
RT "A family of cyclin D homologs from plants differentially controlled
by growth regulators and containing the conserved retinoblastoma
protein interaction motif";
RL Plant Cell 7:85-103(1995).
[2]
RN REVISIONS.
RP Murray J.A.H.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
[3]
RX SEQUENCE FROM N.A.
RC STRAIN=CV, Columbia;
RX MEDLINE=2106719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federapfel N.A., Kaul S.,
White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hlizar L.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Kim C.J., Koo H.L., Kremetska I., Kuriz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
Miltescher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
Utherback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana.";
RL Nature 408:816-820(2000).
-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.

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CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
CC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN-CV. LANDSBERG ERECTA; TISSUE=Seedling;
RC MEDLINE=20063486; PubMed=10617198;
RX MEDLINE=95210930; PubMed=7696881;
RT Soni R., Carmichael J.P., Shah Z.H., Murray J.A.H.;
RT "A family of cyclin D homologs from plants differentially controlled
RT by growth regulators and containing the conserved retinoblastoma
RT protein interaction motif.";
RT Plant Cell 7:85-103(1995).
RN [2]
RP REVISION TO 371.
RA Murray J.A.H.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP STRAIN-CV. COLDIMBIA;
RC MEDLINE=20063486; PubMed=10617198;
RX Mayer K.F.X., Schueller C., Mamuti R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Striekema W., Entian K.-D., Teyryn N.,
RA Harris B., Anstorge W., Brandt P., Givelli L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier L.B., Maché R., Mueller M.,
RA Reichert B., Pottelet D., Puigdomenech P., Watson M., Schmidtmann T.,
RA Kelsch B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohelsel J., Zimmermann W., Weiler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grynoprez B., Chang Y.-J., Vandebussche F.,
RA Braeken M., Weltjens I., Voet M., Bastlaens I., Aert R., Defoor E.,
RA Melzengeneger T., Boche G., Kampsperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveleen M., Dirks W.,
RA Moollman P., Klein Lankhorst R., Rose M., Haut J., Koetler P.,
RA Benneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA de Keyser A., Buyschaert C., Gielen J., Villarroel S., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K., Mayes R.,
RA Pettett A., Rajandream M.A., Lyne M., Benez V., Reckmann S.,
RA Borkova D., Blocker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argüello A., Vitale D., Liqouri R., Piravandi E.,
RA Messner O., Outgley F., Clapaud G., Mwendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Glibons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Punelle B., Bent E., Johnson S., Jacou D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bietel C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Huberman K.,
RA Parnell L., Dehlla N., Gnoj L., Schütz K., Huang B., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cortes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harton G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Marx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kremer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spiehl J., Ryan E., Andrews S., Gelsel C., Layman D.,
RA Du H., Ali J., Bergloff A., Jones K., Prone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
RA Ma P., Zhong Y., Preston R., Vil D., Shekhar M., Matero A., Shah R.,
RA Svaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Granel S., Shohay N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana".
RL Nature 402:769-777(1999).
CC -1 SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).

DR EMBL: X76123; CAA53729.1; -
DR PIR: S41710; S41710.
DR HSSP: P20248; 1PIN.
DR InterPro: IPR000533; Cyclin.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin.C; 1.
DR SMART: SM00385; CYCLIN.C; 2.
DR PROSITE: PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Mitosis.
DR SEQUENCE 441 AA; 49205 MW; B6EAC037C98880A7 CRC64;

Query Match 11.7%; Score 205.5; DB 1; Length 441;
Best Local Similarity 27.2%; Pred. No. 2.6e-11;
Matches 74; Conservative 51; Mismatches 112; Indels 35; Gaps 12;

QY 26 PECSFSDSDSPPPSPPTTEDCYSIASFIEHERNFVPGFEYLRS--FQSRSLDANAREE 82
DB 168 PKEDIVDIDAA-----DYNNDLAVVEVEDMYKFKSAENDSRPHYMDSQPEINEKMR 221
QY 83 S-VGMILKVHAYYGFOPLTAVLAVNYMDRFLDSRRRLPETNGWPLQYVACLSIAAKE 140
DB 222 AILDMLVQVHYKFLSEPLTFLINIVDRYLSK---TTSRRRLQGLGMSMLLSKYE 278
QY 141 EPLVPSLDDQ-IEGAKTIFEPRTIRRMELVGLVDRLSRVSPLCFIAF--ACKYDS 197
DB 279 EIMAEVNDLVICSDGSISNE--QVLRMEKKILGALVLYPTVYVLFVRFKSLSDS 336
QY 198 --TGFFIRLSRATETIIVSNIQESFLAYWPSCTIAAAILTA--ANEIPMSVYKEDN 252
DB 337 DYERKMYFL----AELGMN--ATITMCGSMIAAAVYAROTLNKMPINNETLRMH 390
QY 253 AESWCEGLRKEKVIQCYQLOMELVINNNOKRL 284
DB 391 T-----GFSEVQIMDCAKLIDFHGGSTQDKL 417

RESULT 5
CGB2_MESAU STANDARD: PRT; 397 AA.

ID CGB2_MESAU STANDARD: PRT; 397 AA.
AC P37883;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE G2/mitotic-specific cyclin B2.
GN CGB2.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX Shitaki T., Yamashita K., Nishitani H., Nishimoto T.;
RA Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
CC -----

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DR EMBL: D17294; BAA04127.1; -
DR HSSP: P20248; 1ISU.
DR InterPro: IPR000533; Cyclin.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin.C; 1.
DR SMART: SM00385; CYCLIN.C; 2.
DR PROSITE: PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Mitosis.
DR SEQUENCE 397 AA; 45278 MW; 247DBAA412E6C8BD CRC64;

Query Match 11.4%; Score 201; DB 1; Length 397;
Best Local Similarity 25.4%; Pred. No. 5.9e-11;
Matches 81; Conservative 54; Mismatches 134; Indels 50; Gaps 12;

QY 12 LCGEDSGILGSESPCSFSDSDS-----SPPPSPPTTEDCYSIASFIEHERNFVPGFEYL 67
DB 104 LQAFSDAIL-----CTIEDIDNEDMENPOLCSQYVNDIYQLQLEVASINPHF--- 154
QY 68 SFQSRSLDANAREESVGMILKVHAYYGFOPLTAVLAVNYMDRFLDSRRRLPETNGWPLQ 127
DB 155 --LDGRDINGRRALVMDVQVHSHKFLRDLQETLYMCIALMDRFQADPVCRRK---LQL 209
QY 128 VSVACLSIAAKEEPLVPSLDDQIEGAKYT---FEPRTIRRMELVGLVDMRLRSYT 183
DB 210 VGITMLLLASKYEEMFSPN---IEDFYITDMNVTSSQIEMETLLIKELKEFELGRPL 264
QY 184 PLCLFL--AFACKVQD-STGTFIRFLSRATETIIVSNIQESFLAYWPSCTIAAAILTAAN 240
DB 265 PLHPLRRASKAEVDVEQHTLAKYLM-----LTLIDYDMVNHHPQVAAAASCLSGK 317
QY 241 EI--PNWSYKPEENAESWCEGLRKEKVIQCYQLOMELVINNNOKRLPLIKVLPQ----- 292
DB 318 VLGQGNWNL-----KQYYTYGMEVEVLEVMQMAKNVYKVENILTKFLAVKKNYASRSL 372
QY 293 LNVYTRTRMRSSVTSSESS 311
DB 373 LKISTIPQLNSKTIKDIAS 391

RESULT 6
CGB2_MEDSA STANDARD: PRT; 328 AA.

ID CGB2_MEDSA STANDARD: PRT; 328 AA.
AC P30278;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE G2/mitotic-specific cyclin 2 (B-like cyclin) (Cycw2) (Fragment).
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.
OX NCBI_TaxID=3879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93104677; PubMed=1307238;
RA Hirt H., Mink M., Plosser M., Boegre L., Gyoergye J., Jonak C.,
RA Gartner A., Dudits D., Heberle-Bors E.;
RT "Alfalfa cyclins: differential expression during the cell cycle and
RT in plant organs";
RU Plant Cell 4:1531-1538(1992).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC -----

CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -1- TISSUE SPECIFICITY: ONLY EXPRESSED IN ORGANS WITH DIVIDING CELLS.
 CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
 CC ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X68741; CAA48675.1; -
 DR PIR: S29925; S29925.
 DR PIR: P00490; P00490.
 DR HSSP: P20248; 1J5U.
 DR InterPro: IPR000553; Cyclin.
 DR Pfam: PF00134; cyclin_1.
 DR Pfam: PF02984; cyclin_C_1.
 DR SMART: SM00385; CYCLIN; 2.
 DR PROSITE: PS00292; CYCLINS; 1.
 DR CYCLIN; Cell cycle; Cell division; Mitosis.
 FT NON TER 1
 SO SEQUENCE 328 AA; 37710 MW; 7EACCB166B5D949E CRC64;
 Query Match 11.4%; Score 200; DB 1; Length 328;
 Best Local Similarity 26.6%; Pred. No. 5.6e-11;
 Matches 67; Conservative 41; Mismatches 112; Indels 32; Gaps 9;
 QY 32 DIDSPPPPPTTEDCYSIASFIEHERNFVPGFEYLS---RQSRSLDANAREES--VG 85
 DB 55 DIDSC-----DANNSLAWEYIEDLHAYRKIEYLGCVSPYMDQDLNEMRAILVD 108
 QY 86 WILKYAVYGPQPLAYAVNMDRLDRFLDRLPBTNGMPLOLVSVACLSIAAKMEPLVP 145
 DB 109 WLIEVHDKFDLMQETLEFLVNLIDRLAKQNVVRKK---LQLVGLVAMLLACKYEVSVP 165
 QY 146 SLIDLOIEGAKYIFEPRTIRRMELVLGVLDRLRSVTPICLAF--ACKVDSGTFTIR 203
 DB 166 VVSOL-ITHADRAYTRKDLLEKMLNTLOYNMSLPYAVFMRRLKAAQADKLELVA 224
 QY 204 FLISRATETIVSNIQEASFIAWPSCLIAAAAILTA---ANEIPNMSVYKPEAAESMCEGL 260
 DB 225 FF-----LVDSLIVEYEMLKFPPLSVAAAAYTTAOCIVSGFRHMN-----KTCWHNTY 273
 QY 261 RKEKYIGCYQLM 272
 DB 274 SEDQLLECSMLM 285
 RESULT 7
 CG2B_MEDVA STANDARD; PRT; 434 AA.
 ID CG2B_MEDVA
 AC P46278;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G2/mitotic-specific cyclin 2 (B-like cyclin) (Cycms2).
 OS Medicago varia.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
 OC NCBI_TaxID=36902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. A2;
 RX MEDLINE=953755A1; PubMed=7647566;
 RA Medkline I., Boegre L., Dahl M., Pirck M., Ha D.T.C., Smoboda I.,
 RA Heberle-Bore E., Ammerer G., Hilt H.,
 RT "Cycms3, a novel B-type alfalfa cyclin gene, is induced in the
 RT G0-to-G1 transition of the cell cycle.";

RL Plant Cell 7:759-771(1995).
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 CC (MITOSIS) TRANSITION.
 CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
 CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
 CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
 CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
 CC ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X82040; CAA57560.1; -
 DR HSSP: P20248; 1F1N.
 DR InterPro: IPR000553; Cyclin.
 DR Pfam: PF00134; cyclin; 1.
 DR Pfam: PF02984; cyclin_C_1.
 DR SMART: SM00385; CYCLIN; 2.
 DR PROSITE: PS00292; CYCLINS; 1.
 DR CYCLIN; Cell cycle; Cell division; Mitosis.
 SO SEQUENCE 434 AA; 49367 MW; 644EFOA2681A6C32 CRC64;
 Query Match 11.4%; Score 200; DB 1; Length 434;
 Best Local Similarity 26.6%; Pred. No. 8.3e-11;
 Matches 67; Conservative 41; Mismatches 112; Indels 32; Gaps 9;
 QY 32 DIDSPPPPPTTEDCYSIASFIEHERNFVPGFEYLS---RQSRSLDANAREES--VG 85
 DB 161 DIDSC-----DANNSLAWEYIEDLHAYRKIEYLGCVSPYMDQDLNEMRAILVD 214
 QY 86 WILKYAVYGPQPLAYAVNMDRLDRFLDRLPBTNGMPLOLVSVACLSIAAKMEPLVP 145
 DB 215 WLIEVHDKFDLMQETLEFLVNLIDRLAKQNVVRKK---LQLVGLVAMLLACKYEVSVP 271
 QY 146 SLIDLOIEGAKYIFEPRTIRRMELVLGVLDRLRSVTPICLAF--ACKVDSGTFTIR 203
 DB 272 VVSOL-ITHADRAYTRKDLLEKMLNTLOYNMSLPYAVFMRRLKAAQADKLELVA 330
 QY 204 FLISRATETIVSNIQEASFIAWPSCLIAAAAILTA---ANEIPNMSVYKPEAAESMCEGL 260
 DB 331 FF-----LVDSLIVEYEMLKFPPLSVAAAAYTTAOCIVSGFRHMN-----KTCWHNTY 379
 QY 261 RKEKYIGCYQLM 272
 DB 380 SEDQLLECSMLM 391
 RESULT 8
 CG2B_ARATH STANDARD; PRT; 428 AA.
 ID CG2B_ARATH
 AC P30183; Q42081;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G2/mitotic-specific cyclin (B-like cyclin).
 DE CYC1 OR AR4G37490 OR F6G17.140.
 GN Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 CC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. C24;
 RX MEDLINE=92228771; PubMed=1373494;
 RA Hemerly A.S., Bergounioux C., van Montagu M., Inze D.,

RA Ferrel P.C.G.:
 RT "genes regulating the plant cell cycle: Isolation of a mitotic-like
 RT cyclin from *Arabidopsis thaliana*."
 RL Proc. Natl. Acad. Sci. U.S.A. 89:3295-3299(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RX MEDLINE=2008348; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wamont R., Murphy G., Volckaert G.,
 RA Pohl T., Dueterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansojge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermair B., Maché R., Mueller M.,
 RA Kreis M., Delseny M., Podgornesch P., Watson M., Schmidtlin T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Honelsel J., Zimmermann W., Weiler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Kobbén J.,
 RA Van der Schuren J., Gymnopoulos B., Changu Y.-J., Vandenbussche F.,
 RA Breken M., Welljens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Meltnegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Staveren M., Dirke P.,
 RA Woolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
 RA Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA de Keyser A., Buyschaert C., Gielen J., Villarroel R., de Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McLay K., Mayes R.,
 RA Petzell A., Rajendram M.A., Lyne M., Benes V., Reichmann S.,
 RA Borjova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fatmann B., Granderath K., Dauner D., Herzi A.,
 RA Neumann S., Argüello A., Vitale D., Liquri R., Piravandi E.,
 RA Massenot O., Ougley F., Clabund G., Wundelsh A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lechery A., Aubourg S.,
 RA Chedor F., Cooke R., Berger C., Monfort A., Cascuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
 RA Perez-Perz A., Purrelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bletke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Beyan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedina N., Gnoj L., Schütz K., Huang E., Spiegel L.,
 RA Sekon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Hartom G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Mix P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Speith J., Ryan E., Andrews S., Giesel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antonolu B., Zidan M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodi M., Johnson A.,
 RA Chen E., Marra M., Martenssen R., McCombie W.R.,
 RT "Sequence and analysis of chromosome 4 of the plant *Arabidopsis*
 RT *thaliana*."
 RL Nature 402:769-777(1999).
 RN [3]
 RP SEQUENCE OF 6-94 FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA Phillips G., Gigot C.;
 RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
 CC -I- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 CC (MITOSIS) TRANSITION.
 CC -I- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
 CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
 CC MAURATON PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
 CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -I- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
 CC ABRUPTLY DESTROYED AT MITOSIS.
 CC -I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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[illegible]

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favallo A., Fullon L., Gattung S., Greco T., Kirsten J.,
RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
RA Matlis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D.,
RA Riklen L., Riles L., Tatch A., Trevaskis E., Vignati D.,
RA Wilcox L., Mohlman P., Vaudin M., Wilson R., Waterston R.,
RA Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 PROTEIN KINASE TO
CC FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2 AND ARE
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -!- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED BEFORE MITOSIS. THE
CC LEVELS PEAK LATE IN THE G2 PHASE OF THE CELL CYCLE AND ARE AT A
CC MINIMUM IN G1 PHASE.
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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CC -----
DR EMBL: M65070; AAA34502.1; -
DR EMBL: X62319; CAA44195.1; -
DR EMBL: U40828; AAB68060.1; -
DR PIR: S14166; S14166.
DR HSSP: P20248; IJSD.
DR SGD: S0006323; CLB2.
DR InterPro: IPR000553; Cyclin.
DR Pfam: PF00134; cyclin_C.1.
DR SMART: SM00385; CYCLIN; 2.
DR SMART: PF02984; cyclin_C.1.
DR PROSITE: PS00292; CYCLINS; 1.
DR Cyclin: Cell cycle: cell division; Mitosis; Multigene family.
KW Cyclin: Cell cycle: cell division; Mitosis; Multigene family.
SQ SEQUENCE 491 AA; 56246 MW; B68FF888871022A0 CRC64;

Query Match 11.3%; Score 198.5; DB 1; Length 491;
Best local similarity 25.5%; Pred. No. 1.3e-10;
Matches 84; Conservative 59; Mismatches 119; Indels 67; Gaps 18;

3 VSCISDYDL-----LCGDSGSLGSESPESDIDSSPPPTEDDYASIEHME 57
187 ISIVGELPKPKKVCDENG-----KEVEWEDLDAE-----DVNDPFVSEV--- 230
OY 58 RNFVPGFEYLSR-----FQSRSLDANAREBSVGMILKHAHYGFQPLAYLAV 105
DB 231 -NDI--FEYHOLEVITLPKREDLYOHRNHN--RDILVMVLVKHNKFKELLPETLYLAI 286
OY 106 NVMDRLDLSRLPETNGWPLQVSVACLSAAKEEPLVSLDLIDEGKKYFEPRTR 165
DB 287 NMDREL--GEIVOLD--KQLVGTSCLEFASKYEYSPISIKHFASETGACTEDE--IK 342
OY 166 RMELLYLVGVDMRLSVTPCLFLAFACKVD---STGPIRLISRAHAIIVSNIQEAS 221
DB 343 EGKFKILKTLKFNINPNPNFLRIS--KADDDIDQSRLAKFL-----SI---SLVDFR 394
OY 222 FLAYWPSCIAAAAILTANET--PNMSVVKPENAESGELREKVIK--QYQLMQLVYN 278
DB 395 FGLTSPICAAAMFMGRKMLGKQWD---GNLIHVSGGYTEELAPVHMIMDYLV-- 448
OY 279 NNGRKLPPLVLPQLARTTTRBRSSVTS 307
DB 449 -----SEIVHDEFHKKYQSRFMKASITS 472

RESULT 10
CG21_SOYBN STANDARD; PRT; 454 AA.
ID CG21_SOYBN
AC P25011;
01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 16-mitotic-specific cyclin S13-6 (B-1like cyclin).
OS Glycine max (Soybean)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=CV_AKISNGOKU; TISSUE=Root;
RX MEDLINE=91330894; PubMed=1831125;
RA Hata S., Kouchi H., Suzuki I., Ishii T.,
RT Isolation and characterization of cDNA clones for plant cyclins.";
RL EMBD J. 10:2681-2688(1991).
CC -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
CC (MITOSIS) TRANSITION.
CC -!- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -!- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
CC ABRUPTLY DESTROYED AT MITOSIS.
CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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CC -----
DR EMBL: X62820; CAA44632.1; -
DR PIR: S16522; S16522.
DR HSSP: P30274; IVIN.
DR InterPro: IPR000553; Cyclin.
DR Pfam: PF00134; cyclin_C.1.
DR Pfam: PF02984; cyclin_C.1.
DR SMART: SM00385; CYCLIN; 2.
DR PROSITE: PS00292; CYCLINS; 1.
DR Cyclin: Cell cycle: cell division; Mitosis.
KW Cyclin: Cell cycle: cell division; Mitosis.
SQ SEQUENCE 454 AA; 50094 MW; 34EB4356586A/C10 CRC64;

Query Match 11.2%; Score 197.5; DB 1; Length 454;
Best local similarity 25.9%; Pred. No. 1.5e-10;
Matches 69; Conservative 45; Mismatches 103; Indels 49; Gaps 11;

26 PECFSDDSSPPPPPTT---EDCYSIASFIEHNFVPGFEYLSRFQSRSLDANARE 81
173 PKQIIDLIDASDVNDLAEVYIDIDYKFKVLNENSR---PHDYIG--SQPEINERMA 227
OY 82 ESYGMILKHAHYGPOPLAYLVANVMDRLDLSRLPETNGWPLQVSVACLSAAKME 141
DB 228 ILVDMLIDVHTKFEISLEFLYLITINIDRFLANKYVPRRE---DLQVGSANLMSKYE 284
OY 142 PLVPSILD--IQEGAKYIEPRTIRMEMLYGVDMRLSVTPCLFLAFACKVDSTGT 200
DB 285 IMPEVYNDVCLSDRAVTHE--HILTMKTLINKLEMTLITVPLVFL----- 330
OY 201 FIRELSRATEIIVSNIQESFLA-----YWPSCIAAAAILTA--ANETPNMS 246
DB 331 -VFIRKASVDDQELDNM--AHFISLGMNMYATIAMCPMSVAASAVLAARCTLNKAPFN 387
OY 247 VVKPENAESGELREKVIKGYQLM 272
DB 388 EYIKLHT-----GYSOQLMDCARLL 408

RESULT 11
CG2A_DAUCA STANDARD; PRT; 341 AA.
ID CG2A_DAUCA
AC P25010;
01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE G2/mitotic-specific cyclin C13-1 (A-like cyclin) (Fragment).
 OS *Daucus carota* (Carrot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
 OX NCBI_TaxId=4039;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. KURODAGOSUN;
 RX MEDLINE=91330894; PubMed=1831125;
 RA Hata S., Kouchi H., Suzuki I., Ishii T.;
 RT "Isolation and characterization of cDNA clones for plant cyclins.";
 RL EMOB J. 10:2681-2688(1991).
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 CC (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 AND CDK2 PROTEIN
 CC KINASES TO FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
 CC AND ARE ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X62819; CAA44631.1; -
 CC PIR: S16521; S16521.
 DR HSSP: P20248; IJBU.
 DR InterPro: IPR000553; Cyclin.
 DR Pfam: PF00134; cyclin_1.
 DR SMART: SM00385; CYCLIN_C; 1.
 DR SMART: SM00385; CYCLIN_C; 1.
 DR PROSITE: PS00292; CYCLINS; 1.
 KW Cyclin; Cell cycle; Cell division; Mitosis.
 FT NON_TER 1
 SQ SEQUENCE 341 AA; 38724 MW; 5708DF4269C06F3F CRC64;
 Query Match 11.2%; Score 196.5; DB 1; Length 341;
 Best Local Similarity 26.4%; Pred. No. 1.3e-10;
 Matches 77; Conservative 44; Mismatches 122; Indels 49; Gaps 11;
 QY 10 DLICGEDSSGILSGESPEC-----SFSDDSSPPPTTEDCYSIASF 53
 DB 32 DLICRE-----FEVPKCYAOKRRKRGVDEGVDEKFPDPOKMSAYSDVYEYLKQ 84
 QY 54 IEHERNFVPGFEXLSRPOSHSLDANAREESVGLIKVHAYVGFQPLTAYLVANVMDRFLD 113
 DB 85 MEMETKRPRPMNYIEQV-KDVTSMNMGVLVMDLVEVSLKLPETLYLAISVDRYLS 143
 QY 114 SRRLPEINGPVLQVSVACSLAAKMEPLVPSLLDQIGAKYIFEPRIIRRELLVYG 173
 DB 144 VNVJL---NRQKLDLAGVSSFLASKYEIRPKNVADF-VITDWTYSQOEVVAKMEADLLK 199
 QY 174 VLDMRLSVYPLCFELAF-ACKVDSTGTPIRFLISRATETIIVSIOASFLAYW-----P 227
 DB 200 TLFEKMSPTVKTFGLGIRAVOENPDVPIKLF-----EFLANTYLAELSLIDYCLEFEP 253
 QY 228 SCIAAAAILTAANEI-PN---WSVVKPENASWCEGLRKEKVIQCYQLMOEL 275
 DB 254 SLTAASVTLARFTIRNVNPMST-----ALOKCSGYKSKNDKRCVLLIHL 300.
 RESULT 12
 CG2B_ORYSA STANDARD; PRT; 419 AA.
 ID CG2B_ORYSA
 AC Q40671;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G2/mitotic-specific cyclin 2 (B-like cyclin) (Cycos2).
 OS *Oryza sativa* (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoae; Oryza.
 OX NCBI_TaxId=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. PIN GAEM 53;
 RX MEDLINE=95261415; PubMed=7742859;
 RA Sauter M., Mehmedov S.L., Kende H.;
 RT "Gibberellin promotes histone H1 kinase activity and the expression
 RT of cdc2 and cyclin genes during the induction of rapid growth in
 RT deepwater rice internodes.";
 RL Plant J. 7:623-632(1995).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=CV. PIN GAEM 53;
 CC Sauter M.;
 CC "Isolation and characterization of a cDNA encoding a mitotic cyclin of
 CC the Cyc2 type from rice.";
 CC (In) Plant Gene Register PGR97-001.
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 CC (MITOSIS) TRANSITION.
 CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
 CC SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
 CC MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
 CC SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
 CC ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X82036; CAA57556.1; -
 CC HSSP: P20248; IJBU.
 DR InterPro: IPR000553; Cyclin.
 DR Pfam: PF00134; cyclin_1.
 DR Pfam: PF02984; cyclin_C; 1.
 DR SMART: SM00385; CYCLIN_C; 1.
 DR SMART: SM00385; CYCLIN_C; 1.
 DR PROSITE: PS00292; CYCLINS; 1.
 KW Cyclin; Cell cycle; Cell division; Mitosis.
 FT NON_TER 1
 SQ SEQUENCE 419 AA; 47572 MW; A8774B56BD839A5B CRC64;
 Query Match 11.2%; Score 196.5; DB 1; Length 419;
 Best Local Similarity 26.6%; Pred. No. 1.7e-10;
 Matches 72; Conservative 43; Mismatches 123; Indels 33; Gaps 9;
 QY 20 ILSESEPCSFSDSSPP-PSPTTEDCYSIAFIHERNFVGFYLS-----RFS 72
 DB 128 VMGSELKEIEMEDIEEAPDIDSCDANNSLAIVVEYISFYRRSGLSCVSPNMLSQ 187
 QY 73 RSLDANAREESVGLIKVHAYVGFQPLTAYLVANVMDRFLDPSRLPETNGPVLQVSVAC 132
 DB 188 NDINEKAKGIIIDWLIIEHYKLELDELFLTVMIIDFLARENVYKK---LDLVGYTA 244
 QY 133 LSLAAKMEPLVPSLLDQIGAKYIFEPRIIRRELLVGLVDMRLSVYPLCFELAF- 191
 DB 245 MLACKYEEVSVYVEDI-ILICORATRTDILEMERIYVTLQFDSVPPYPCFMREL 303
 QY 192 -ACRVDTGTGFIIRFLISRATETIIVSIOASFLAWPSCIAAAAILTAANEIPMWVVKP 250
 DB 304 KAAQSKKLEIMSF-----IIEISLIVEYEMLKFOPSMLAAAIYAQCTINGF----- 352
 QY 251 ENAESW---CE---GLRKEKVIQCYQLMOEL 275
 DB 304 KAAQSKKLEIMSF-----IIEISLIVEYEMLKFOPSMLAAAIYAQCTINGF----- 352

DB 353 ---KSNWKCCELHTYXSEQLMECSKMWEL 380

RESULT 13

ID CG21_YEAST STANDARD: PRT: 471 AA.

AC P24868;

DT 01-MAR-1992 (Rel. 21, Created)

DT 01-MAR-1992 (Rel. 21, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE G2/mitotic-specific cyclin 1.

GN CLB1 OR SCB1 OR YGR108W OR G5967.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE-91191554; PubMed-1849457;

RA Surana U., Robitach H., Price C., Schuster T., Fitch I., Futcher A.B.,

RA Nasmyth K.;

RT "The role of CDC28 and cyclins during mitosis in the budding yeast S.

RT cerevisiae.";

RL Cell 65:145-161(1991).

RN (2)

RP SEQUENCE FROM N.A.

RX MEDLINE-91191555; PubMed-1849458;

RA Chikara J.B., Richardson H.E., Sugimoto K., Henze M., Lew D.J.,

RA Wittenberg C., Reed S.I.;

RT "A cyclin B homolog in S. cerevisiae: chronic activation of the Cdc28

RT protein kinase by cyclin prevents exit from mitosis.";

RL Cell 65:163-174(1991).

RN (3)

RP SEQUENCE FROM N.A.

RA Medler H., Scharfe M., Medler E., Wambutt R.;

RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M

CC (MITOSIS) TRANSITION. INTERACTS WITH THE CDC2 PROTEIN KINASE TO

CC FORM MPF. G2/M CYCLINS ACCUMULATE STEADILY DURING G2 AND ARE

CC ABRUPTLY DESTROYED AT MITOSIS.

CC -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED BEFORE MITOSIS. THE

CC LEVELS PEAK LATE IN THE G2 PHASE OF THE CELL CYCLE AND ARE AT A

CC MINIMUM IN G1 PHASE.

CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.

CC

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DB 189 EXEMDDE-----EDC-DDPLAWSEEVNDI--FDYHHEITITLPKANLYKHKN 236

QY 80 -----REESGWLTKHAYVYQFPLAVLVNMDRFLDSRRLPEFNGPILQVYASCL 135

DB 237 IKONPDILVNIWIKTHKHNKGLPETLYALINMDRFL--CEEVQVLN--RLQVGTSCLE 293

QY 136 AKMEPELVPSL--LDLQEGAKYFEPRTIRMBELVGLVMDRLRSVTPCLAFAPAC 193

DB 294 ASKEEYIYSPSIKHNAYEEDGACV---EDIKEGEFLIEKIDPDISFANPNFARRIS- 349

QY 194 KVDSTGTFIRELISRAETIYSNIQESAFSLAVPSCIAAAILTANET--PNMSVAPRE 251

DB 350 KADVDYDSRTLAKFLMETI---SIVDFKIGILPISLCASAAFLSRKMKIGKTMW----G 402

QY 252 NAESECEGRKREKVGICQVQMLVYINN 279

DB 403 NLHYSGGYTKAKLYPCQLMDYLVGS 430

QY

DB

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27 EGSFSDIDSSPPPTTEDCYSIASFIEHNFVPGFEYLSRFRSRLDANA----- 79

Query Match 11.2%; Score 196.5; DB 1; Length 471;

Best Local Similarity 27.6%; Pred. No. 1.9e-10;

Matches 74; Conservative 42; Mismatches 111; Indels 41; Gaps 12;

27 EGSFSDIDSSPPPTTEDCYSIASFIEHNFVPGFEYLSRFRSRLDANA----- 79

DR EMBL: AF002822; MAD09309.1; -

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CC

DR EMBL; AB020981; BAA78387.1; -
 DR EMBL; AL080146; CAB45739.1; -
 DR HSSP; P20248; 1J5U.
 DR MIM; 602755; -
 DR InterPro; IPR000553; Cyclin.
 DR Pfam; PF00134; cyclin.1.
 DR Pfam; PF02984; cyclin.C.1.
 DR SMART; SM00385; CYCLIN; 2.
 DR PROSITE; PS00292; CYCLINS; 1.
 DR CYCLIN; Cell cycle; Cell division; Mitosis.
 KW SEQUENCE 398 AA; 45281 MW; 874466E1DD6844C4 CRC64;
 SQ

Query Match 11.1%; Score 196; DB 1; Length 398;
 Best Local Similarity 26.5%; Pred. No. 1.7e-10;
 Matches 83; Conservative 45; Mismatches 119; Indels 66; Gaps 13;

QY 12 LCGESSGLISESPCSDDSDS-----SPPPSPTTECCYSLASIEHEERNVPEFEYL 67
 DB 105 LCGESSGLISESPCSDDSDS-----SPPPSPTTECCYSLASIEHEERNVPEFEYL 155
 QY 68 SRFQSRSDANAREESVGLKVAHYGQPLAYLVNVMRELD-----SRRLPPTNGM 123
 DB 156 --LDGNDINGRRMALLVDLVVHNSKFRLLQETLYMCVIMDFLOVQVYSRK----- 206
 QY 124 PLOYSVACLSIAKMEEPFLVPSLIDQIEGAKYI-----FEPTIRMEILVGLDWR 179
 DB 207 KIQLVGTLALLASKKEEFPSPN-----IEDFYITDNAVTSQIRMEILILKELFEL 261
 QY 180 RSVTPLCFL--AFFACKVD-STGTFTFLISRATETIVSNIOASFLAVWPCIAAAIL 236
 DB 262 GRPLPFLHFRRAASKAGEVDEQHTLAKYLME-----LTLIDYDVHYHPSVAAAASC 314
 QY 237 TIANEL--PMSVYKPEANSCGIRKEKVIQCYLOMELVINNR----- 282
 DB 315 LSKQVVGQGRKWNL-----KQQYTYGTENEVEVMQMAKNVKNENLTKEITAKKYA 369
 QY 283 --KLPLKVLPL 293
 DB 370 SSKLKISMTPL 382

RESULT 15
 CG21_ANTMA STANDARD; PRT; 473 AA.
 ID CG21_ANTMA
 AC P34800;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G2/mitotic-specific cyclin 1.
 OS Antirrhinum majus (Garden snapdragon).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Veronitaceae; Antirrhinum.
 OX NCBI_TaxID=4151;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94148008; PubMed=8333906;
 RA Robert P.R., Coen E.S., Murphy G.J.P., Doonan J.H.;
 RT "Patterns of cell division revealed by transcriptional regulation of
 RT genes during the cell cycle in plants.";
 RL EMBO J. 13:616-624(1994).
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 CC (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADILY DURING G2
 CC AND ARE ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SUBUNIT: INTERACTS WITH THE CDK2 AND CDK2 PROTEIN KINASES TO FORM
 CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
 CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
 CC ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
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 CC -----

DR EMBL; X76122; CA53728.1; -
 DR PIR; S41709; S41709.
 DR HSSP; P30274; 1VIN.
 DR InterPro; IPR000553; Cyclin.
 DR Pfam; PF00134; cyclin.1.
 DR Pfam; PF02984; cyclin.C.1.
 DR SMART; SM00385; CYCLIN; 2.
 DR PROSITE; PS00292; CYCLINS; 1.
 DR CYCLIN; Cell cycle; Cell division; Mitosis.
 KW SEQUENCE 473 AA; 52704 MW; 502CF173558763BA CRC64;
 SQ

Query Match 11.1%; Score 194.5; DB 1; Length 473;
 Best Local Similarity 26.8%; Pred. No. 3e-10;
 Matches 62; Conservative 44; Mismatches 104; Indels 21; Gaps 8;

QY 45 EDCYSIASFIEHRNFVPGFEYLSRFQSRSDANAREESVGLKVAHYGQPLAYYA 104
 DB 196 EDNYKRYKSYENSR---PHDYG--SQPEINEMKRAILLDVLVYHHKELSPETLYL 250
 QY 105 VNYMDFLDSRLPETNGWPLQVSVACLSIAKMEEPFLVPSLIDQIEGAKYIPEPT 164
 DB 251 INVYDRYASE---TIRRELQVIGAMLIASKYEIRWAPVEHEL--VCISDNTYSDKQ 306
 QY 165 RMELLVGLDWRLLNSVPLCLAFPAQVDSGTGIFRFLISRATETIVSNIOEASFLA 224
 DB 307 LVMEKRTIGALEWYLVLPFYVFLVRF--IKASMTDSVEMVYFLAELGMNNT--ATLT 362
 QY 225 YWPCIAAAILTA---ANETPMNSVYKPEANASWCEGLRKEVIGCYQLM 272
 DB 363 YCPSMIAASVYARCTLNAPFMNETHQLHT-----GFSEPOLMCAKLL 408

Search completed: October 23, 2002, 14:38:29
 Job time : 15 secs


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Db      1  MSLSCSDCFCFDLLCGEDSNITFISGGDDDLPEYT -SDVESIP-----TDVDESIAGLLED 53

QY      57  ERNFVPEFETLSRQSRSLDANNAKRESVGMILLKVAHYGFGPOLTXYLVANMDPEFLDSRR 116

Db      54  ERD-IAGVN-----SSSSSNVDSSYTRSTSTAMILLKVGORTYGFOLYLVAVSTFEDRLNAHH 110

QY      117  LPETNGWPLDVSVACISLAKAKKEBPVPSLLDLQIEGAKYTFEEDRTIRRMELLVGLVD 176

Db      111  LPKTNGWPQDLSVACISLNAKKEESVPSLLDLQIEGANFTFEEDRNRIORRELLVRLYID 170

QY      177  WRKLSVPLGFLFAEFACKYDSTGTFLIRFLISRTATEIVSINIOEASFGLVWPSGCIAMAIL 236

Db      171  WRKLSISFPCLSFLFAKIDPDTGTYIGFELTRAKELLISTVGETSLIERBPCIAAMAML 230

QY      237  TAANEIPWVSVKPEKNAESWCESGLIRREKYIGCYQLMOELVINNOBKRLPLEKVLPEQRYT 296

Db      231  SSANDLPFESFTTQOHAEMACDCGILHMDINASCITKLIOGESNNRPKOP--KVLPOLRYM 288

QY      297  TTRTRRSSTVSFSSSSSTFSLSCKRRKLNNTLAWDDGNS 338

Db      289  TRASTLASS-----ESSSTSSSPYKRRKRLNNNSRRADDKES 325

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ID	PRELIMINARY;	PRT;	372 AA.
P93103			
DC	P93103;		
DT	01-MAY-1997 (TRIMBLrel. 03, Created)		
DT	01-MAY-1997 (TRIMBLrel. 03, Last sequence update)		
DT	01-DEC-2001 (TRIMBLrel. 19, Last annotation update)		
DE	CYCLIN-D LIKE PROTEIN.		
GN	CYCD1.		
OC	Chenopodium rubrum (Red goosefoot) (Pigweed).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Eumariophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.		
OX	NCBI_TaxID=3560;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Renx A., Fountain M., Beck E.;		
RT	"Nucleotide sequence of a cDNA encoding a D-type cyclin from a		
RT	photoautotrophic cell suspension culture of Chenopodium rubrum L.";		
RL	Plant Physiol. 0:0-0(0).		
CC	-I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.		
DR	EMBL: Y10162; CAA71244.1; "		
DR	Interpro: IPR004366; Cyclin.		
DR	Interpro: IPR004367; Cyclin_C.		
DR	Pfam: PF00134; cyclin; 1.		
DR	Pfam: PF02984; cyclin_C; 1.		
DR	SMART: SM00385; CYCLIN; 1.		
DR	PROSITE: PS00292; CYCLINS; 1.		
KW	Cell cycle; Cell division; Cyclin.		
SQ	SEQUENCE 372 AA; 41768 MW; 655D1C91A5DB17CF CRC64;		
Query Match	26.4%; Score 463.5; DB 10; Length 372;		
Best Local Similarity	31.7%; Pred. No. 2.8e-38;		
Matches 120; Conservative	66; Mismatches 116; Indels 77; Gaps		
QY	9 YDLGCEDSGILGSESPCESFSDISSPPSPTEECYSI-----50		
DB	5 FDLGCEMDSI-----FDEVDMN--YGVVDDVDVLICMLQOQHGNLRNFDEFTL 53		
QY	51 -----ASFIEHKNFYGFEYLSRFORSRLDANARESV 84		
DB	54 ILIIIKHNFEALISGFVANHECLASLDNERQHFLGLDYILKFRNGDLDLGARMLV 113		
QY	85 GWLKYHAYYGEOPLTAYLVAVNYMDRFLDSRLRLEPTNQNPLQIVSVACLSIAKMEPLV 144		
DB	114 DWIKYQSHNFEPLCVLYSVNYLDRLFSAYELP--GRAMAMQLGLVACTSLAAVDETIV 172		
QY	145 PSLDLQISEAKITFEPRITRMELLVYGLVDMRLRSTPTLCFLAFACKYDSGTITRF 204		
DB	173 PLIDLVQSSKVFPAKTIQRMELLVSTLKMRSQVSTPSFIDVLYKLISGDKMPSKS 232		

[illegible]

ID	Q9ZRX9	PRELIMINARY:	PRT:	354 AA.
AC	Q9ZRX9			
DT	01-MAY-1999	(TREMBLrel. 10, Created)		
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DE	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
GN	CYCCLIN D2.1	PROTEIN.		
OS	Nicotiana tabacum (Common tobacco).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.			
NCBI	NCBI_TaxID=4097;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99097070; PubMed=9880377;			
RA	Sorell D.A., Combettes B., Chabuet-Gigot N., Gigot C., Murray J.A.H.,			
RT	"Distinct Cyclin D Genes Show Mitotic Accumulation or Constant Levels			
RL	of Transcripts in Tobacco Bright Yellow-2 Cells."			
CC	Plant Physiol. 119:343-350(1999).			
DR	-I- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.			
DR	EMBL; AJ011892; CAA09852.1; "			
DR	Interpro: IPR004366; cyclin_C.			
DR	Interpro: IPR004367; cyclin_C.			
DR	Pfam: PF00134; cyclin_1.			
DR	Pfam: PF02984; cyclin_C; 1.			
DR	SMART; SM00385; CYCLIN; 1.			
DR	PROSITE; PS00292; CYCLINS; UNKNOWN_1.			
KW	Cell cycle; Cell division; Cyclin.			
QO	SEQUENCE 354 AA: 39714 MW: 18363A0E78689BF CRC64;			
QY	Query Match	26.1%;	Score 458.5;	DB 10; Length 354;
	Best Local Similarity	36.0%;	Pred. No. 8.4e-38;	
	Matches 120;	Conservative 63;	Mismatches 127;	Indels 23; Gaps
Db	5 CLSDYDLGCEBDSGILSGSPCSFSD-IDSSPPPPSPPT-TEDCYSASFIEHNFYP 62			
	23 CFDDVDSLTTSQOQ--IETKSKDISFNGIRSEPLIDPPLSECLSF--MYGRKEHFLP 78			
QY	63 GFEILSRFQSRSLDANARESVGMILKVAHYVGFOPLTAYLAANYMDRFLDSRLPETNG 122			
Db	79 KDQYVELRLRGDDLDLSRKALDMLIKAHNHYGELGSLFCLSYNYDRFLSLVELPRSKT 138			
QY	123 WPIQDVSVAQLSLAAKKEEPLVDSLDLQIEGAKYIREPTIRRMELLYGVYDMLRSY 182			
Db	139 WTVQLLAVACLSLAAKKEEINVLPTVLDLQVGDPEFVEGKTIOEMELLYSLTKRWQAY 198			
QY	183 TPLCLFLAFPAKVDSTGTGTFIRFLISRAKTEITIVSNICDASPLAWPSCIAAAILITANE 242			
Db	199 TPTFTIDYFMKKNMGDQIPSRHPLISGSMODLSTIIRSIDLPEFRSSIASVAMVSGET 258			
QY	243 PNMVSVVPEANESCEGIRKEKVGCVQLMOELVYNNORKPLPLTKVLPQ-----LRVTT 297			
Db	259 QAKDIDA--MPCFFIHLDKGRVQKVELLIDLT-TLTITTAASLIVPSPIGVLEAA 315			
QY	298 RTMRSS--TVSFFSSSSSTFSLGCKRRKLN 327			
Db	316 CLSTKSGDERTVGCTTSSHT-----KRRRLD 342			


```

RESULT 4
095XN7 PRELIMINARY: PRT: 368 AA.
ID 095XN7;
AC 095XN7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NTCYC3-1 PROTEIN.
GN NTCYC3-1
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.

RA Sekine M.;
RT "Cell cycle regulated gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
EMBL: AB015222; BAA76478.1; -
DR InterPro: IPR004366; Cyclin.
DR InterPro: IPR004367; Cyclin_C.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin_C; 1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLINS; UNKNOWN_1.
KW Cell cycle; Cell division; Cyclin.
SO SEQUENCE 368 AA; 42827 MW; CDF280F183601808 CRC64;

Query Match 24.4%; Score 429.5; DB 10; Length 368;
Best Local Similarity 34.7%; Pred. No. 7.5e-35;
Matches 104; Conservative 56; Mismatches 123; Indels 17; Gaps 4.

24 RESPECSFSDSPPPSPPTTE-DCY---SIASFIEHRNVVPGPEVLSRQSHSDAN 78
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
30 ETIEDEIEIEKEATPLPLPLEODLFWEDEELSLFTKEKETISNFT--KIDPLCL 86
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
79 ARESVGWILKHAVYGFQPLTAVLVNMDRFLDSRLPETNGPVLQVSVACISLAAK 138
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
87 SRKEAVKMTILKANVAGYGFSTFAILAIINFDRLSLHPQKXKPMWILQVAVTCLSLAAK 146
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
139 MEELPVSLDDQIEGAKYIEFPRTIRRELLVGLVDMRLSVYPLCLAFACKVSDST 198
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
147 VETQVPLPLDDQVEDAKVFEAKTIQRELLVLSLKWKNMPVPLSFVDHIIIRLGLK 206
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
199 GFPIRFLSRAREIIVSNIOEASFVLAWPSCIAAAAILTAANEIPMWSVFNENASWCE 258
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
207 SHIHNEFLKQCRHILLVLAOCRFLSYMPSVATATMLHVIHQVECNADVQONOLLEVL 266
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
239 GLRKEKRYIGCYQLMDELVINNNOKRLPLIKVLPQLRVTRTRMRSSVSSSSSTFS 318
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
267 NISKERVNDYDELTVEVSYSNISHK-----RKYESPINSPSAVIDTFVSSSENSNES 317
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
092RX8 PRELIMINARY: PRT: 373 AA.
ID 092RX8;
AC 092RX8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CYCLIN D3.1 PROTEIN.
GN CYCD3.1
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.

```

[illegible]

Query Match 24.1%; Score 423.5; DB 10; Length 343;
 Best Local Similarity 33.6%; Pred. No. 2.7e-34;
 Matches 111; Conservative 56; Mismatches 128; Indels 35; Gaps 4;

QY 4 SCLSDYDLICGDDSSGIISSGESPECSFSDIDSSPPPTTEEDCYSTASFTIEHERNVPW 63
 DB 40 SPLLKHDLLICGVDD-----DDKKEELSLCKEEOE-----70
 QY 64 FEYLSNFSRSLDANARESVGMILKHAHYGFOPLTAYLANVMDRFLDSRLPETNGW 123
 DB 71 YELRYLEENPSLAKRADAVEEMERFVIGYFSALTNALAVNYDRFLCTFOQDKPW 130
 QY 124 PLQVSVACLSIAAKMEELVPSLLDLQIEGAKYIFEPRTIRMEELVGLVDMRLRSYT 183
 DB 131 MQLAAVACLSIAAKVEEYQVLLDLQVEESKYFESTIORMELVSLTKKMNFPYT 190
 QY 184 PLCLAFPCACKYDSTGTFRFLISRATETIVSNIOBASFLAWPSCIATAALITLANEIP 243
 DB 191 PISFLEYIARRLALSKSHLCKEFLNCECLISLITDCRFMCHPSALATATWLYISSIE 250
 QY 244 NMSVYPEAAESMCEGLREKRYIGCYOLMOELVI-----NNORKLPILKVPOLRVTTR 298
 DB 251 PCIGVYQULINILINKKVECKKLQEVATSVHSGNKKRFGSLIPSKGVNDIS 310
 QY 299 TRMRSS-TVSSFSSSSTSPSLCKRRKLN 327
 DB 311 FSCDSWPLDSTAVSSSPEHLSKRIKTON 340

RESULT 7

Q9FKP7 PRELIMINARY; PRT; 308 AA.
 AC Q9FKP7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE D-TYPE CYCLIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN 11
 RC SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE:98344145; PubMed:9679202;
 RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
 RT features of the regions of 1,381,565 bp covered by twenty one
 RT physically assigned p1 and TAC clones.";
 RL DNA Res. 5:131-145(1998).
 DR EMBL: AB011479; BAB11564.1; -
 DR InterPro: IPR004366; CYCLIN.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; UNKNOWN_1.
 KW CYCLIN.
 SQ SEQUENCE 308 AA; 34715 MW; 96PD929C868DD62F CRC64;

Query Match 23.9%; Score 420.5; DB 10; Length 308;
 Best Local Similarity 34.6%; Pred. No. 4.8e-34;
 Matches 100; Conservative 53; Mismatches 95; Indels 41; Gaps 7;

QY 8 DYDLGGE---DSSGILSGS-----PECSFSDIDSSPPPTTEEDCYSTASFTIEHER 58
 DB 7 ELSLCTESVWDEGMIVDETPLEISTPQMGFSQSESE-----ITMENWEKK 55
 QY 59 NFVPEEYLSRFQSRSLDAN-AAESVGMILKHAHYGFOPLTAYLANVMDRFLDSRLT 117
 DB 56 QHLPDSDDYIKRLRSGLDLNVRGRDLNMIWKACEVHQGPCLFCIAMNYIDRFLSVHL 115
 QY 118 PETNGPDLVSVACLSIAAKMEELVPSLLDLQIEGAKYIFEPRTIRMEELVGLVDM 177

DB 116 PSGKWLLOLLAVACLSIAAKIEETEVPMLIDLOVGDPOEFAKSVORMELLVNLKW 175
 QY 178 RLRSVTPCLCLAF-----ACKVDSTGTFRFLISRATETIVSNIOBASFLAWPSCI 232
 DB 176 RLRLITPQSTIRYLRKMSKODQEPNT-----LISRLQVIASTTKIDLERPSEVAA 231
 QY 233 AAILTANAEI-----PNMSVYKPEAAESMCEGLREKRYIGCY 270
 DB 232 AVALISGELORVHFNDSFSLSLQKERYKKIGMISDSDLSQ 280

RESULT 8

Q9FGQ7 PRELIMINARY; PRT; 367 AA.
 AC Q9FGQ7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE CYCLIN D3-LIKE PROTEIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN 11
 RC SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."
 RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AB025614; BAB09645.1; -
 DR InterPro: IPR004366; CYCLIN.
 DR SMART: SM00385; CYCLIN; 1.
 DR PROSITE: PS00292; CYCLINS; UNKNOWN_1.
 SQ SEQUENCE 367 AA; 42351 MW; 9D26B28A66152C54 CRC64;

Query Match 23.9%; Score 419.5; DB 10; Length 367;
 Best Local Similarity 35.7%; Pred. No. 7.7e-34;
 Matches 107; Conservative 57; Mismatches 101; Indels 35; Gaps 7;

QY 55 EHERNFPGEFYLSRFSRSLDANARESVGMILKHAHYGFOPLTAYLANVMDRFLDS 114
 DB 76 ENETNPFCEGEOILLDGL-----VSCRKALDMVLRYKSHYGTSLTALILAVNYFDRMETS 130
 QY 115 RLRLPTNGPLOIVSVACLSIAAKMEELVPSLLDLQIEGAKYIFEPRTIRMEELVGLV 174
 DB 131 IRLQTRKPMQSLVAVASLSIAAKVEEYQVLLDLQVEEARYFEAKTIQRMELLST 190
 QY 175 LDWRLSYTPLCF-----LAFPCACKYDSTGTFRFLISRATETIVSNIOBASFLAWPSCI 230
 DB 191 LQWRHVPYTPISFPDHLIRRGSKWHQGLDFCR-----KCEKLLSVLADTRFMKYPFSLV 246
 QY 231 AAAAILTANAEIPKMSVYKPEAAESMCEGLREKRYIGCYOLMOELVYNNORKLPILKVL 290
 DB 247 ATAIMILVEELKPCDEVEYQSIITTLKYNQEVNVECY-----ELLEHNSKKRMMNLV 302
 QY 291 PQ-----LRVTRTRMRSSSTVSSFSSTSPSLCKRRKLN-----NRLMVD 333
 DB 303 DDDSGVGLDDDDSSNSMNVSTTASVSSSSSPEPL-LKRRRVQDOOMRLPSINRFLD 361

RESULT 9

Q9XFR7 PRELIMINARY; PRT; 308 AA.
 AC Q9XFR7;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE D-TYPE CYCLIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

RA Ishida J., Jiang P. X., Jones T., Kamiya A., Karlin-Neuman G.,
RA Kawai J., Iam B., Lee J. M., Lin J., Liu S. X., Matlin-Neuman G.,
RA Nguyen M., Onodera C. S., Palm C. J., Pham P. K., Quach H. L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C. C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R. W., Theologis A.,
RT Boker J. R.,
RT "Arabidopsis cDNA clones",
RT Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC - SIMILARITY: BELONGS TO THE CYCLIN FAMILY.
DR EMBL: AL132978; CAB62115.1; -
DR EMBL: AT052653; AAK36569.1; -
DR InterPro: IPR004366; Cyclin.
DR InterPro: IPR004367; Cyclin_C.
DR InterPro: IPR003880; Phosphopent_attach.
DR Pfam: PF00134; cyclin; 1.
DR Pfam: PF02984; cyclin.C; 1.
DR SMART: SM00385; CYCLIN; 1.
DR PROSITE: PS00292; CYCLINS; UNKNOWN_1.
DR PROSITE: PS00012; PHOSPHOPENTATTACHIN; UNKNOWN_1.
KW Cell cycle; Cell division; Cyclin.
KW SEQUENCE 361 AA; 41737 MW; DBBE9329A339D02 CRC64;

Query Match 23.4%; Score 411; DB 10; Length 361;
Best local Similarity 31.4%; Pred. NO. 5.4e-33;
Matches 109; Conservative 59; Mismatches 119; Indels 60; Gaps
7;
QY 6 LSDYDLACEDSDSGILSGSPSCPSFSDIDSSPPSPPTTEDCPSIASFIEHNFVCPFE 65
DB 49 LSDHDLMDDELSTLISKQEPCLYDEI-----LDD-----E 80
QY 66 YLSRFQSRSLDANAREESGATLKNAHYGQPIATLAVNAYNDRLPDSRLRPETNGWPL 125
DB 81 FL-----VLCRKALDWTFKKSHYGNSTLTALLAVNVEFDRFTTSKRFOTDKPMS 131
QY 126 QLVSVACLSLAAMEEPPLPSLLDQIGAYFIEFPTIRRMELLYGVLDMLRSVTP 185
DB 132 QVLAFLACSLAAKVEIRNPFLDQVEARVVEAQTIONMELLYVSTLDWMHNPVPI 191
QY 186 CPTAFACKYVDSTGTFIRFLISRATETIYSIQEASFLAWPSCIAAAILTANAEIPMW 245
DB 192 SFPDHTRIRRSFKSHQLEFLSRCESLSTLSTIPSRFLSPSVLAIAVSVIRDLKMC 251
QY 246 SVVCKPMAASWCEGKJRKKEVIGCYQLOMELVINNNORKPLPLKVLPP-----LVATRTTGM 301
DB 252 DEAVYQSQMLTKLTKYDSEVAKCY-----ELVLDHSPPSKRRMMKMQQASPFGVDPASP 307
QY 302 RSTVSSFSSSSSTFSLS-----CKRRKLN-----NRLMVD 333
DB 308 SDSNESWVYASASVSSSPSEPLKRRRVEQOMRLSINRMFFD 354

RESULT 11
Q9SMD4 PRELIMINARY: PRT; 336 AA.
AC Q9SMD4
DT 01-MAY-2000 (TREMBLrel. 13, Created)
OC 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CYCD3_3 PROTEIN.
GN CYCD3_3.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. UC82B;
RX MEDLINE=20566012; PubMed=11131518;
RA Karimben A., Yao J. L., Zhan X., O'Brien I., Morris B.;
RT "Isolation of three distinct CycD genes expressed during fruit
development in tomato".
RT J. Exp. Bot. 51:1789-1797(2000).
RL

GenCore version 5.1.3
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OK protein - protein search, using sw model

Run on: October 23, 2002, 14:37:34 ; Search time 13 Seconds

(Without alignments)
636,944 Million cell updates/sec

Title: US-09-665-308D-12

Perfect score: 1758

Sequence: 1 MSVSCLSDYDLGEGDSSGT.....SKRRRLNRLNLTDDKGNSE 339

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRNUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	180.5	10.3	432	1	US-08-522-166-8	Sequence 8, Appl
2	180.5	10.3	432	1	US-08-488-382A-8	Sequence 8, Appl
3	180.5	10.3	432	2	US-08-480-912-8	Sequence 8, Appl
4	177.5	10.1	295	2	US-08-464-517-19	Sequence 19, Appl
5	177.5	10.1	295	2	US-08-246-361A-19	Sequence 19, Appl
6	177.5	10.1	295	3	US-08-463-772-19	Sequence 19, Appl
7	177.5	10.1	295	5	PCT-US93-05000-2	Sequence 19, Appl
8	177.5	10.1	295	5	PCT-US93-05000-19	Sequence 19, Appl
9	177.5	10.1	309	2	US-08-464-517-4	Sequence 4, Appl
10	177.5	10.1	309	3	US-08-463-772-4	Sequence 4, Appl
11	176.5	10.0	289	2	US-08-246-361A-4	Sequence 4, Appl
12	176.5	10.0	289	5	PCT-US93-05000-4	Sequence 4, Appl
13	173.5	9.9	662	2	US-08-770-761A-5	Sequence 5, Appl
14	173.5	9.9	705	2	US-08-770-761A-7	Sequence 7, Appl
15	171.5	9.8	295	1	US-07-947-120-8	Sequence 8, Appl
16	171.5	9.8	295	1	US-08-472-893A-8	Sequence 8, Appl
17	171.5	9.8	295	2	US-08-460-694-2	Sequence 2, Appl
18	171.5	9.8	295	3	US-08-460-744-2	Sequence 2, Appl
19	171.5	9.8	295	3	US-07-667-711B-2	Sequence 2, Appl
20	171.5	9.8	295	3	US-08-947-492-8	Sequence 8, Appl
21	171.5	9.8	618	2	US-08-770-761A-3	Sequence 3, Appl
22	171.5	9.8	647	2	US-08-770-761A-8	Sequence 8, Appl
23	171.5	9.8	660	2	US-08-770-761A-2	Sequence 2, Appl
24	171.5	9.7	150	2	US-08-460-694-3	Sequence 3, Appl
25	171.5	9.7	150	3	US-08-460-744-3	Sequence 3, Appl
26	171.5	9.7	150	3	US-07-667-711B-3	Sequence 3, Appl
27	170	9.7	236	2	US-08-464-517-22	Sequence 22, Appl

28	170	9.7	236	2	US-08-246-361A-22	Sequence 22, Appl
29	170	9.7	236	3	US-08-463-772-22	Sequence 22, Appl
30	170	9.7	236	5	PCT-US93-05000-22	Sequence 22, Appl
31	169.5	9.6	295	2	US-08-464-517-2	Sequence 2, Appl
32	169.5	9.6	295	2	US-08-246-361A-2	Sequence 2, Appl
33	169.5	9.6	295	3	US-08-463-772-2	Sequence 3, Appl
34	167.5	9.5	295	2	US-08-464-517-20	Sequence 20, Appl
35	167.5	9.5	295	2	US-08-246-361A-20	Sequence 20, Appl
36	167.5	9.5	295	3	US-08-463-772-20	Sequence 20, Appl
37	167.5	9.5	295	5	PCT-US93-05000-20	Sequence 20, Appl
38	167	9.5	292	2	US-08-464-517-23	Sequence 23, Appl
39	167	9.5	292	2	US-08-246-361A-6	Sequence 6, Appl
40	167	9.5	292	2	US-08-246-361A-23	Sequence 23, Appl
41	167	9.5	292	3	US-08-463-772-23	Sequence 23, Appl
42	167	9.5	292	5	PCT-US93-05000-23	Sequence 23, Appl
43	165	9.4	492	1	US-08-463-090B-10	Sequence 10, Appl
44	162.5	9.2	291	5	PCT-US93-05000-6	Sequence 6, Appl
45	160	9.1	404	2	US-09-092-770-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-522-166-8
Sequence 8, Application US/08522166
Patent No. 5783661
GENERAL INFORMATION:
APPLICANT: ROBERTS, J.M.; Ohtsuo, M; Koff, A.C.; Cross, F.
TITLE OF INVENTION: Human Cyclin E
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
City: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44mb storage
COMPUTER: IBM PC Compatible/Pentium
OPERATING SYSTEM: MS-Windows 3.1
SOFTWARE: Word for Windows-6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/522,166
FILING DATE: June 7, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,309
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Sheinness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHRO-1-8597
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
TELEFAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-522-166-8
Query Match 10.3%; Score 180.5; DB 1; Length 432;
Best Local Similarity 29.3%; Pred. No. 3.3e-12;
Matches 75; Conservative 31; Mismatches 101; Indels 49; Gaps 10;

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QY 16 DSSGLISESEGCFSFDIDSSPPPTTECCYASIAFIEHERNFVGFELISFQSRSL 75
Db 159 DMSVLEDEKRP-----VSYNENP-----DYHEDIHYLLR--EMEYCKCKRKGVMKK--QPD1 2068
QY 76 DANAREBSVGILKVHAYVYGFQPLTAVLAAYMYMDRFLDSRRRLPBTGNSMPLDLYSVACLST 139
Db 207 TNSMKAIIYDMLVEGEYEEKYQKNFTLHLAVYIDRFELSSMSVLRGK---LQIVGTAAML 263
QY 136 AAKKEEPLVSLDLQIEGAKYI----FEPTIRRMELVYGVDMRLRSTVPLCELAFF 191
Db 264 ASKEEELIYPPVAEF-----YITDDPYTKQVIRMBELVLYKLTFTDLAPVYNQFLTQY 318
QY 192 -----ACKVDSTGTFIRLIRLSPATELIVSNIDIASFLVWPSCIAAAAILTPANEIPN 244
Db 319 FLHOOPANCKYVESLAMELIGEL-----SLIDADPYLKYLPVINGAFAHLLALYIV-- 367
QY 245 MSVYKPEMAESWCEGL 260
Db 368 -----TGQSMPESL 376

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      RESULT 2
US-08-488-382A-8
Sequence 8, Application US/08488382A
Patent No. 5807698
GENERAL INFORMATION:
APPLICANT: Roberts, J.M.; Ohitsuho, M.; Koff, A.C.; Cross, F.
TITLE OF INVENTION: Human Cyclin E
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-3.5 inch, 1.44mb storage
COMPUTER: IBM PC Compatible/Pentium
OPERATING SYSTEM: MS-Windows 3.1
SOFTWARE: Word for Windows-6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,382A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,309
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHRO-1-8600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0735 (direct)
TELEFAX: 1-206-224-0779
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Cyclin B polypeptide sequence; Figure 3
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
US-08-488-382A-8
Query Match          10.3%; Score 180.5; DB 1; Length 432;
Best Local Similarity 29.3%; Pred. No. 3,3e-12;
Matches 75; Conservative 31; Mismatches 101; Indels 49; Gaps 10;

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Db 159 DMSIVLDEK-----VSNENP-----DYHEDHITYLKR--EMEYKCKPKVGYMMK--QpDI 206

QY 76 DANAREESVGLKLVHAYIGFQPIFLATLAYLVNMDRFLDSRRLEPBTNGWPLQIVASCLSL 135
Db 207 TNSMKAIIIVDMVLVEGGEYKIKQNETLHLAVNYIDRFSSMSVLRGK---LQIVGTAMML 263

QY 136 AAKMEPLVSLDLQIQEGAKYI---FEPPTIRRMELVLGVDMVRSVPPLCFAPF 191
Db 264 ASKEPEIIPPEYAEF-----YTIIDDYTKQVLRMHLVLKVLTFPLAAPTVOEFTQY 318

QY 192 -----ACKVDSTGTETIRFLIRLIRATEFIYSNIOEASFLAYWPSCLAAAIILTAANEIPN 244
Db 319 FLHQOPANCKVESSLAMFLGEL-----SLIDADADLYKVLPSVLVIGAFAHIALYTV-- 367

QY 245 MSYVKPENAESWCEGL 260
Db 368 -----TGOSWPESSL 376

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OY 76 DANAREESGILKAVHYGFOPLAVYAVNYMDRFLDSRLPBNNGWPLQVSVACLSTL 135
DB 207 TNSMNAIILVDMLEVEGEYKQLONEFLHLAVNYIDRFLSMSGVLRG---LQVGNAMLL 263
OY 136 AKKHEEPLVPSLIDQIGAKYI---FEPRTRMELLYGLVDMRSLVPLCLAF 191
DB 264 ASKEEYIPPEVAEF---VYTDYTKKQVLRMEHLVLYKLFIDLAAPIVNGFLQY 318
OY 192 -----ACKVDSGTFTIRFLISRATEIIVSNIQASFLAYPSCIAAAIITANEIN 244
DB 319 FLHQOPANCKVESLAMEFGEEL-----SLIDADPYLKYPVYAGAFHIALYTV--- 367
OY 245 WSVVKNPENASWCEGL 260
DB 368 -----TGQSWPEST 376

RESULT 4
US-08-464-517-19
; Sequence 19, Application US/08464517
; Patent No. 5869640
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHYE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,517
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mathew P. Vincent
; REGISTRATION NUMBER: 36,709
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-517-19

Query Match 10.1%; Score 177.5; DB 2; Length 295;
Best Local Similarity 25.2%; Pred. No. 4e-12;
Matches 56; Conservative 45; Mismatches 108; Indels 13; Gaps 6;
OY 50 IASIEHERNFVPGFEYLSRFSQSLDANAREESGILKAVHYGFOPLAVYAVNYMD 109
DB 28 LRAMKAETCAPSVSYFCVQKEVL-PSMRKIVATWMLVECEBQKCEBEVPLAMNYLD 86

OY 110 RFLDSRLPBNNGWPLQVSVACLSTLAKMEE--PLVPSLIDQIGAKYIFPRTRM 167
DB 87 RFLSLPEVKKSR---LQLGATCMFVASKRKETIPLTAERLCITYDGS---IRPEELQW 140
OY 168 ELVLYGLVDMRLRSLVPLCLAFPAACKVDSTGTFIRFLISRATEIIVSNIQASFLAYWP 227
DB 141 ELLVLYKLLKWNLAAMTPHDFIEHFLSKMPAEENKQIIRKHAOTFVALCATDVKFTISNP 200
OY 228 SCIAAAIITANEINPMSVKNPENASWCEGLR-KEKYIGC 268
DB 201 SWVAGSVVAA---VKGLMLRSPNNFLSYRLRFLRSRYIKC 239

RESULT 5
US-08-246-361A-19
; Sequence 19, Application US/08246361A
; Patent No. 5998582
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHYE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,361A
; FILING DATE: 19-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mathew P. Vincent
; REGISTRATION NUMBER: 36,709
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 295 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-246-361A-19

Query Match 10.1%; Score 177.5; DB 2; Length 295;
Best Local Similarity 25.2%; Pred. No. 4e-12;
Matches 56; Conservative 45; Mismatches 108; Indels 13; Gaps 6;
OY 50 IASIEHERNFVPGFEYLSRFSQSLDANAREESGILKAVHYGFOPLAVYAVNYMD 109
DB 28 LRAMKAETCAPSVSYFCVQKEVL-PSMRKIVATWMLVECEBQKCEBEVPLAMNYLD 86
OY 110 RFLDSRLPBNNGWPLQVSVACLSTLAKMEE--PLVPSLIDQIGAKYIFPRTRM 167
DB 87 RFLSLPEVKKSR---LQLGATCMFVASKRKETIPLTAERLCITYDGS---IRPEELQW 140

TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millita Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL91-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-05000-19

Query Match 10.1%; Score 177.5; DB 5; Length 295;
Best Local Similarity 25.2%; Pred. No. 4e-12;
Matches 56; Conservative 45; Mismatches 108; Indels 13; Gaps 6;

QY 50 IASFIENHNFVPGFEYLSRFSRSIDANAREESVGMILKVAHYGQPLFYLAVENTMD 109
DB 28 IRLAKAEETCAPSVSYFCYQKEVL-PSMKRIATVMTLEVCBEKCEEPFLAMNYLD 86
QY 110 RLDSRLLEPTNGWPLQVSVACSLAAKME--PLVPSLDLQIEGAKYFEPTIRRM 167
DB 87 RLSTLEPVAKSR---LQILGATCMFVASKMETIPLTAEKLCITYDGS--IRPELLQM 140
QY 168 ELIVGLVLMRLSVTPPLCFELAFACKVDSTGTFRFLISRATETIIVSNIDQASFLAWP 227
DB 141 ELLLVKLMNLAAMPHPFIHFILSKMPEABENKQIIRKHAQTVALCANDVKTISNPP 200
QY 228 SCIAAAAILTAANEIIPNMSVVRPENAESWCEGLR-KEVYIGC 268
DB 201 SMVAAGSVAA---YKGLNLRSPPNMFLSYRLTRFLRSVYIKC 239

RESULT 9
US-08-464-517-4
Sequence 4, Application US/08464517
Patent No. 5869640
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,517
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308
FILING DATE: 16-OCT-1992
APPLICATION NUMBER: US 07/888,178
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,514
FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIT-004C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-517-4

Query Match 10.1%; Score 177.5; DB 2; Length 309;
Best Local Similarity 25.6%; Pred. No. 4.3e-12;
Matches 69; Conservative 43; Mismatches 139; Indels 19; Gaps 8;

QY 39 PPSPTTE-DCYSIASFIENHNFVPGFEYLSRFSRSIDANAREESVGMILKVAHYGQ 97
DB 36 PRLAMELCEHVP-VRREERYLPQCSYKCYO-KDIQPYMRMVAWTMLEVCBEKCE 93
QY 98 PLTVAVLVNVDRLDRLSRRLPETNGWPLQVSVACSLAAKME--PLVPSLDLQIEGA 155
DB 94 EYEPFLAMNYDRLVAGVPPPKSH--LQLLGAVCMFLASKIKETSPLETKLCITYDNS 150
QY 156 KYTEPPTIRMEELVYGVDMRLRSVTPPLCFELAFACKVDSTGTFRFLISRATETIYS 215
DB 151 ---IKPOLLEWELVGVGKLMNLAATVPDFTFHLIRKLPQOREKLSIRKHAQTFIAL 207
QY 216 NIOEASFLAWPSCIAAAAILTAANEIIPNMSVVRPENAESWCEGLR--EKVIGCYQLMQ 273
DB 208 CATPFRAMYPSPMIALGSGAALCGLODEEVSLSLGDALTELAKITMTVDCLAKQ 267
QY 274 ELVINNNOKRLPLKVLPLQRLVTTTRTMR 303
DB 268 D-----QIEAVLINSIQYRQDQDGSKS 291

RESULT 10
US-08-463-772-4
Sequence 4, Application US/08463772
Patent No. 6066501
GENERAL INFORMATION:
APPLICANT: BEACH, David H.
TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM: Floppy disk

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/05000
FILING DATE: 19930525
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,178
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSH191-02A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 616-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US93-05000-4

Query Match 10.0%; Score 176.5; DB 5; Length 289;
Best Local Similarity 26.3%; Pred. No. 5e-12;
Matches 66; Conservative 39; Mismatches 129; Indels 17; Gaps 6;

QY 57 EENFPGFVLSRFSRLDANARESGWILKVAHYGPPPLTAIYLVNMDRFLDSRR 116
DB 34 EERYLQGSYFKCVQ-KDIQPYMRMVAFTMLEVCEBQCEEVPLAMNLDLDFLGVP 92
QY 117 LPEWMPLOIVSACLSLAAMEE--PLVPSLDLQLEGAKYIEPRTIRRMELVGV 174
DB 93 TKSH---LQILGAVCMFLASKETSPLEAKLCITYDNS---IKPELLEWELVYLGK 146
QY 175 LDMRLSVPPLCELAFFACKVDSTGTFIRFLISRATETIYVNIQASPLAIVPSCIAAA 234
DB 147 LKNNLAATVPHDFIEHLIKLPQOREKLSLIRKHAQFTALCAIDFKPAMPPSMIATGS 206
QY 235 ILTANETIPNMSVYKPENAESWCEGLRK--EKVIGCYOLMOELVINNNRLLPLKVLPO 292
DB 207 VGAAICGLQDDEVSLLNCDAITELLAKITWVDVCLAKCE-----QIHAVLVLSLQ 260
QY 293 LKVTTRTRRS 303
DB 261 YRQDDRDSKS 271

RESULT 13

US-08-770-761A-5
Sequence 5, Application US/08770761A
Patent No. 5814503
GENERAL INFORMATION:
APPLICANT: Kovacevic, Steven
APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,761A

FILING DATE: 19-DEC-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-376-0756
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 662 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-770-761A-5

Query Match 9.9%; Score 173.5; DB 2; Length 662;
Best Local Similarity 23.7%; Pred. No. 4.4e-11;
Matches 63; Conservative 52; Mismatches 136; Indels 15; Gaps 7;

QY 6 LSDYDLGCGDSGILSGSPCSFSDIDSPPTTDCYSIASFIEHERNFVPGFE 65
DB 18 ISEEDLVVRGSLAMEHQLLCCEVETIRAVPDANLNDRV--LRAMKAETCAPSVS 75
QY 66 YLSRFSRLDANARESGWILKVAHYGPPPLTAIYLVNMDRFLDSRRLEPENGRL 125
DB 76 YFKCVQKEVL-PSMKRIYATVMTMLEVCEBQCEEVPLAMNLDLDFLEPKRS--L 131
QY 126 QLVSVACLSLAAMEE--PLVPSLDLQLEGAKYIEPRTIRRMELVGVLDMLRSVT 183
DB 132 QILGACMEVASKMETIPLTAELKLCITYDNS---IRPELLQWELLVNKLNNLAAMT 188
QY 184 PLCELAFFACKVDSTGTFIRFLISRATETIYVNIQASPLAIVPSCIAAAILTRANETP 243
DB 189 PHDFIEHLPSKMEAEENKQIIRKHAQFTALCAIDVAFISNPPSVAGSVAA--VQ 245
QY 244 MMSVYKPENAESWCEGLR--KEVIGC 268
DB 246 GLNLRSPNNFLSYRLTRFLSRVYK 271

RESULT 14

US-08-770-761A-7
Sequence 7, Application US/08770761A
Patent No. 5814503
GENERAL INFORMATION:
APPLICANT: Kovacevic, Steven
APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 19-DEC-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-10136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-376-0756
TELEFAX: 317-277-1917
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-770-761A-7

Query Match
Best Local Similarity 23.7%; Pred. No. 4.8e-11;
Matches 63; Conservative 52; Mismatches 136; Indels 15; Gaps 7;

9.9%; Score 173.5; DB 2; Length 705;
Best Local Similarity 23.7%; Pred. No. 4.8e-11;
Matches 63; Conservative 52; Mismatches 136; Indels 15; Gaps 7;

QY 6 LSPYDLCCGDDSGILSGSPSPSDIDSSPPPTTEDCYSTASFIHERNRVPGFE 65
DB 32 ISEEDLLVPRGSLAMEHQLCCVEETIRRAYPDANLNDV--LRAMIKAEETCAPSVS 89
QY 66 YLSRFQSRSIDANAREESVGMILKVHAYYGFOPLTAYLVNMYDRFLDSRRLPETNGMPL 125
DB 90 YKCVQKEVL-PSMRKIVATWMLVECEBCKEVEFPLAMNYLDRLFLEPYKRSR--L 145
QY 126 QLVSAVACLSIAAKME--PLVPSLDLDQIEGAKYIFEPRTIRRMELVLCVLDMLRSYT 183
DB 146 QLGACMCFVASKKKEITPLTAEKLCITYDNS--IRPELLQMLLNNKLNKMLAMT 202
QY 184 PLCEFLAFACKVSTGTFIRFLISRATETIIVSNIGASFLAVWPSCIAAAILITANEIP 243
DB 203 PHDFIEFLSKMPEAEENKQIIRKHAQTFVALCATDVKRFISNPSVMAAGSVAA--VQ 259
QY 244 NMSVVRPENAESWCEGLR-KEKYIGC 268
DB 260 GLNLRSPPNLFSLYRLRFLSRVYIKC 285

RESULT 15
US-07-947-120-8
Sequence 8, Application US/07947120
Patent No. 5538846
GENERAL INFORMATION:
APPLICANT: Meeker, Timothy C.
TITLE OF INVENTION: BCL-1 Locus Nucleic Acid Probes and
NUMBER OF INVENTIONS: Assay Methods
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: Stewart Street Tower, 18th Fl., One Market
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,120
FILING DATE: 19920917
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: 91-210-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-777-9257
TELEFAX: 415-543-4219
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 295 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-947-120-8

Query Match
Best Local Similarity 24.8%; Pred. No. 2e-11;
Matches 55; Conservative 45; Mismatches 109; Indels 13; Gaps 6;

9.8%; Score 171.5; DB 1; Length 295;
Best Local Similarity 24.8%; Pred. No. 2e-11;
Matches 55; Conservative 45; Mismatches 109; Indels 13; Gaps 6;

QY 50 IASFIHERNFVPGFEYLSRFQSRSIDANAREESVGMILKVHAYYGFOPLTAYLVNMYD 109
DB 28 LRAMIKAEETCAPSVSYFKCVQKEVL-PSMRKIVATWMLVECEBCKEVEFPLAMNYLD 86
QY 110 RFLDSRRLPETNGMPLQVSAVACLSIAAKME--PLVPSLDLDQIEGAKYIFEPRTIRRM 167
DB 87 RFLSLEPYKRSR--LQILGATCMFVASKKKEITPLTAEKLCITYDNS--IRPELLQML 140
QY 168 ELVLCVLDMLRSYTPPLCTLAFAACKVSTGTFIRFLISRATETIIVSNIGASFLAVW 227
DB 141 ELLLVNKLKNNLAMPHPDFIEHFLSKMPEAEENKQIIRKHAQTFVALCATDVKRFISNP 200
QY 228 SCIAAAILITANEIPNMSVVRPENAESWCEGLR-KEKYIGC 268
DB 201 SMVAGSVAA--VQGLNRSPPNLFSLYRLRFLSRVYIKC 239

Search completed: October 23, 2002, 14:39:51
Job time: 14 secs